

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 40.2691 Seconds  
(without alignments)  
1899.367 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAFGRWRPPPPPLLLLLLV.....AAEFKLXQAKHDTVLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002.\*

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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 3001  | 98.3        | 570    | 22 | Human membrane or  |
| 2          | 2883  | 94.4        | 541    | 20 | Amino acid sequenc |
| 3          | 1744  | 57.1        | 582    | 22 | Amino acid sequenc |
| 4          | 1742  | 57.0        | 582    | 21 | Hydrophobic domain |
| 5          | 1742  | 57.0        | 582    | 21 | Human isomerase ho |
| 6          | 1606  | 52.6        | 388    | 20 | Amino acid sequenc |
| 7          | 1399  | 45.8        | 441    | 20 | Amino acid sequenc |
| 8          | 1354  | 44.3        | 434    | 21 | Human pancreatic c |
| 9          | 831   | 27.2        | 166    | 23 | Human ovarian anti |
| 10         | 760   | 24.9        | 1241   | 22 | Novel human diagno |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 11 | 743   | 24.3 | 366 | 21 | AA571114 | Human prostate can |
| 12 | 737   | 24.1 | 316 | 20 | AAV23884 | Amino acid sequenc |
| 13 | 651   | 21.3 | 127 | 22 | AA05027  | Human polypeptide  |
| 14 | 309   | 10.1 | 216 | 22 | AB64697  | Drosophila melanog |
| 15 | 297   | 9.7  | 131 | 22 | AAU87239 | Novel central nerv |
| 16 | 291   | 9.5  | 129 | 22 | AAU87542 | Novel central nerv |
| 17 | 291   | 9.5  | 129 | 22 | AAU43542 | Human polypeptide  |
| 18 | 291   | 9.5  | 129 | 22 | AAU19949 | Human human calciu |
| 19 | 270   | 8.8  | 138 | 22 | AB69722  | Drosophila melanog |
| 20 | 268   | 8.8  | 219 | 20 | AAW88556 | Secreted protein e |
| 21 | 268   | 8.8  | 219 | 22 | ABW50323 | Human secreted pro |
| 22 | 268   | 8.8  | 222 | 21 | AAW44249 | Human PRO1304 prot |
| 23 | 268   | 8.8  | 222 | 21 | AAW44868 | Amino acid sequenc |
| 24 | 268   | 8.8  | 222 | 21 | AAW93391 | Human PRO1304 (UNQ |
| 25 | 268   | 8.8  | 222 | 21 | AAW66140 | Protein of the inv |
| 26 | 268   | 8.8  | 222 | 22 | AAW50988 | Human PRO1304 prot |
| 27 | 259.5 | 8.5  | 159 | 21 | AAW10995 | Arabidopsis thalia |
| 28 | 259.5 | 8.5  | 163 | 21 | AAW10994 | Arabidopsis thalia |
| 29 | 256   | 8.4  | 211 | 20 | AAW41706 | Human PRO381 prote |
| 30 | 256   | 8.4  | 211 | 20 | AAW01458 | Polypeptide fragme |
| 31 | 256   | 8.4  | 211 | 21 | AAW44262 | Human PRO381 (UNQ3 |
| 32 | 256   | 8.4  | 211 | 21 | AAW44021 | Human PRO381 prote |
| 33 | 256   | 8.4  | 211 | 21 | AAW33463 | Human PRO381 prote |
| 34 | 256   | 8.4  | 211 | 21 | AAW94975 | Human secreted pro |
| 35 | 256   | 8.4  | 211 | 22 | AAU12363 | Human PRO381 polyp |
| 36 | 256   | 8.4  | 211 | 22 | AAW50909 | Human PRO381 prote |
| 37 | 256   | 8.4  | 211 | 22 | AAW50952 | Human PRO381 prote |
| 38 | 253   | 8.3  | 146 | 21 | AAW39838 | Arabidopsis thalia |
| 39 | 253   | 8.3  | 152 | 21 | AAW39837 | Arabidopsis thalia |
| 40 | 253   | 8.3  | 153 | 21 | AAW39836 | Arabidopsis thalia |
| 41 | 249.5 | 8.2  | 186 | 20 | AAW01459 | Polypeptide fragme |
| 42 | 247   | 8.1  | 146 | 21 | AAW5732  | Arabidopsis thalia |
| 43 | 247   | 8.1  | 152 | 21 | AAW5731  | Arabidopsis thalia |
| 44 | 247   | 8.1  | 153 | 21 | AAW5730  | Arabidopsis thalia |
| 45 | 245.5 | 8.0  | 163 | 23 | ABG60082 | Human DITHP polype |

#### ALIGNMENTS

#### RESULT 1

AAW88320  
ID AAW88320 standard; Protein; 570 AA.

AC AAW88320;

XX 23-MAY-2001 (first entry)

DT Human membrane or secretory protein clone P8EC0007.

DE Human; secretory protein; membrane protein; vaccine; gene therapy;

KW rheumatoid arthritis; diabetes.

XX Homo sapiens.

PN EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.

PR 11-JAN-2000; 2000JP-0118775.

PR 02-MAY-2000; 2000JP-0183766.

(HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

DR N-PSDB; AAF93747.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in

gene therapy or as candidate target molecules in drug development -  
 Claim 1; SEQ ID 8; 609pp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

Sequence 570 AA;  
 Query Match 98.3%; Score 3001; DB 22; Length 570;  
 Best Local Similarity 98.9%; Pred. No. 1.7e-282;  
 Matches 562; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 MAFRGWRPPPPPLLLLLWVTGQAPVAGLSDAELQIERRFVDPDECPTVRSGDFVRYH 60  
 1 MAFRGWRPPPPPLLLLLWVTGQAPVAGLSDAELQIERRFVDPDECPTVRSGDFVRYH 60  
 61 YVGFDPDQKSSYDRDSTNFVKGQLTGMQALVGMVGNRRFVKIPPKLAYNE 120  
 61 YVGFDPDQKSSYDRDSTNFVKGQLTGMQALVGMVGNRRFVKIPPKLAYNE 120  
 121 RVSGVIPPNSVLFHFDVLLMDIWNSEDQVQIHTYFPPSPCRITQVSDFRVHYNGTFLDG 180  
 121 GVSGVIPPNSVLFHFDVLLMDIWNSEDQVQIHTYFPPSPCRITQVSDFRVHYNGTFLDG 180  
 181 TLFDSHNRMTYDYVIGWMLIPGMDKGLLGMVGEKRIITIPPLAYGEDGDKDIPG 240  
 181 TLFDSHNRMTYDYVIGWMLIPGMDKGLLGMVGEKRIITIPPLAYGEDGDKDIPG 240  
 241 QASLVDFVALLDLHNPDKSISTENKVPENCERISQSGDFLTYHYNGTLLDGTLPDSSYS 300  
 241 QASLVDFVALLDLHNPDKSISTENKVPENCERISQSGDFLTYHYNGTLLDGTLPDSSYS 300  
 301 RNRFTDYTGQYVTPGMDGLLVCIGEKRIIVPPHLYGGEGRNIPGSVAVLFDIH 360  
 301 RNRFTDYTGQYVTPGMDGLLVCIGEKRIIVPPHLYGGEGRNIPGSVAVLFDIH 360  
 361 VIDFHNPSDSISITSHYKPPDCSVLSKRGDYLLKHYNASLLDGTLLDSTWNLGKTYNIVL 420  
 361 VIDFHNPSDSISITSHYKPPDCSVLSKRGDYLLKHYNASLLDGTLLDSTWNLGKTYNIVL 420  
 421 GSGQVVLGMDGLRMCVGEKRTVLIIPPHLYGGEAGVGEVPGSAVLFDIEXELVAGL 480  
 421 GSGQVVLGMDGLRMCVGEKRTVLIIPPHLYGGEAGVGEVPGSAVLFDIEXELVAGL 480  
 481 PEGYMFVWNGEVSPLFEIDKDGNGEVLLEFSEYIIHAQVASKGKLAPGDAELIVKN 540  
 481 PEGYMFVWNGEVSPLFEIDKDGNGEVLLEFSEYIIHAQVASKGKLAPGDAELIVKN 540  
 541 MFTNDRNGDGKVTAEFFKLKQDEAKHD 568

Db 541 MFTNDRNGDGKVTAEFFKLKQDEAKHD 568

RESULT 2  
 AAY23886  
 ID AAY23886 standard; Protein; 541 AA.  
 XX  
 AC AAY23886;  
 XX  
 DT 21-SEP-1999 (first entry)  
 XX  
 DE Amino acid sequence of a FK506 binding protein.  
 XX  
 KW Human; FK506 binding protein; FKBP65; immune system disorder;  
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
 KW blood coagulation disorder; blood platelet disorder; wound;  
 KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
 KW hypersensitivity; blood group incompatibility; organ rejection;  
 KW graft versus host disease; inflammatory condition;  
 KW ischemia-reperfusion injury; endotoxin lethality; arthritis;  
 KW complement-mediated hyperacute rejection; nephritis; lung injury;  
 KW inflammatory bowel disease; Crohn's disease; infection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09935160-A1.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 06-JAN-1999; 99WO-US00120.  
 XX  
 PR 09-JAN-1998; 98US-0070875.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Moore PA, Ruben SM, Wei Y;  
 XX  
 DR WPI; 1999-430382/36.  
 DR N-PSDB; AAX36147.  
 XX  
 PT New nucleic acids encoding human FK506 binding proteins  
 XX.  
 PS Claim 12; Fig 3; 87pp; English.  
 XX  
 CC The present sequence represents human FK506 binding protein 65 (FKBP65).  
 CC The polypeptide or polynucleotide may be useful in treating deficiencies  
 CC or disorders of the immune system, by activating or inhibiting the  
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune  
 CC cells. They may be useful in treating or detecting deficiencies or  
 CC disorders of hematopoietic cells, to increase differentiation and  
 CC proliferation of hematopoietic cells including the pluripotent stem  
 CC cells, in an effort to treat those disorders associated with a decrease  
 CC in certain types of hematopoietic cells. They can be used to modulate  
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood  
 CC coagulation disorders, blood platelet disorders or wounds resulting from  
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
 CC strokes or scarring. They can also treat autoimmune disorders, allergic  
 CC reactions and conditions such as asthma (particularly allergic asthma) or  
 CC other respiratory problems, anaphylaxis, hypersensitivity to an antigenic  
 CC molecule, or blood group incompatibility, organ rejection or graft versus  
 CC host disease, inflammatory conditions, both chronic and acute, including  
 CC inflammation associated with infection, ischemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,  
 CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel  
 CC disease, or Crohn's disease. They can also be used to treat viral,  
 CC bacterial, fungal and parasitic infections.  
 XX  
 SQ Sequence 541 AA;  
 Query Match 94.4%; Score 2883; DB 20; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-271;  
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFRGWPPPPPLLLLLLWVTGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYH 60  
DB 1 MAFRGWPPPPPLLLLLLWVTGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYH 60  
QY 61 YVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNE 120  
DB 61 YVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNE 120  
QY 121 RVSGVILPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDFRVHYNGTFLDG 180  
DB 121 RVSGVILPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDFRVHYNGTFLDG 180  
QY 181 TLFSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKOIPG 240  
DB 181 TLFSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKOIPG 240  
QY 241 QASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFLTYYHNGTLLDGLTFLDSSYS 300  
DB 241 QASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFLTYYHNGTLLDGLTFLDSSYS 300  
QY 301 RNRFTDTYIGQYVTPGMDGLGVCIGEKXIVVPHLGYGEGRGNIIPGSAVLVFDIH 360  
DB 301 RNRFTDTYIGQYVTPGMDGLGVCIGEKXIVVPHLGYGEGRGNIIPGSAVLVFDIH 360  
QY 361 VIDFNPSDSISITSHYKPPDCSVLSKKGYLKYHYNASLLDGLTLLDSTWNLGKTYNIVL 420  
DB 361 VIDFNPSDSISITSHYKPPDCSVLSKKGYLKYHYNASLLDGLTLLDSTWNLGKTYNIVL 420  
QY 421 GSGQVVLGMDGLREMCVCEKRTVILPPLHGYGAGVGEVPGSAVLVFDIEKLELVAGL 480  
DB 421 GSGQVVLGMDGLREMCVCEKRTVILPPLHGYGAGVGEVPGSAVLVFDIEKLELVAGL 480  
QY 481 PGYMFVWNGEVSPLFEIDKDGNGEVLLBEFSEYIHAQVAGSGKGLAPGDAELIVKN 540  
DB 481 PGYMFVWNGEVSPLFEIDKDGNGEVLLBEFSEYIHAQVAGSGKGLAPGDAELIVKN 540  
QY 541 M 541  
DB 541 M 541  
RESULT 3  
AAG79226  
ID AAG79226 standard; Protein; 582 AA.  
AC AAG79226;  
XX  
DT 03-JAN-2002 (first entry)  
DE Amino acid sequence of neurotrophic factor expression-inducing agent.  
XX Human; neurotrophic factor; PSEC56; nerve growth factor;  
KW neurite outgrowth; neural disease; dementia; cerebral embolism;  
XX spinal injury; peripheral nerve disease.  
OS Homo sapiens.  
XX  
PN W0200173024-A1.  
XX  
PD 04-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-JP02768.  
XX  
PR 31-MAR-2000; 2000JP-0101300.  
XX  
PA (HELI-) HELIX RES INST.  
PA (WELF-) WELFIDE CORP.  
XX  
PI Mitsumori C, Morikawa N, Hayashi K, Nagahari K, Ota T, Hio Y;  
PI Nishikawa T, Isogai T, Kawasaki M, Hashimoto K, Kishimoto T;  
XX  
DR WPI; 2001-616501/71.

DR N-PSDB; AAI65835.  
XX Neurotrophic factor expression-inducing agent, applicable in developing  
PT drugs for neural diseases e.g. dementia, cerebral embolism, spinal  
PT injury and peripheral nerve diseases by screening their regulatory  
PT effect  
XX  
PS Example 1; Page 34-38; 42pp; Japanese.  
XX  
CC The present sequence represents a human neurotrophic factor  
CC expression-inducing agent. The polypeptide is designated PSEC56.  
CC The PSEC56 protein is used to increase nerve growth factor providing  
CC neurite outgrowth effect, which is applicable in developing drugs for  
CC neural diseases e.g. dementia, cerebral embolism, spinal injury and  
CC peripheral nerve diseases, with use of PSEC56 as the neurotrophic  
CC factor expression-inducing agent which can be applied in a system to  
CC study induction and secretion mechanism of neurotrophic factor.  
XX  
SQ Sequence 582 AA;  
Query Match 57.1%; Score 1744; DB 22; Length 582;  
Best Local Similarity 56.4%; Pred. No. 2.7e-160; Indels 22; Gaps 7;  
Matches 326; Conservative 99; Mismatches 131;  
QY 10 PP-----PLLLLLWVT-----GQAAPVAGLSDAELQIERFVDECPRTVRSQD 55  
DB 6 PPSHLLRLPLQLLLLLLVQAVGRGLGRASPAGGPLED--VVIERYHIPRACPREVQMGD 63  
QY 56 FVRHYVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKL 115  
DB 64 FVRHYNGTFFDQKQFSSYDRNTLVAIVVGVRLLITGMDRGLGCMVNERRLIVPPHL 123  
QY 116 AYGNERVSGVTPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDFRVHYNG 175  
DB 124 GYGSYGLAGLIPDPAFLYFDVLLDWNKEDTVQSTLLRPHPCPRWQDGFVRHYNG 183  
QY 176 TFLDGTFLDSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDG 235  
DB 184 TLLDGTFFDTSYSGGTYYTVGSGWLLKGMQDQGLGCMVGEKRIITIPPLAYGKGYG 243  
QY 236 KDIPQASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFLTYYHNGTLLDGLTFL 295  
DB 244 TVIIPQASLVFVHLITDVHNPKDAVQLETLPLPPGCVRRAGAGDFRHYNGSLMDGLTFL 303  
QY 296 DSSYSNRNRTDTYIGQYVTPGMDGLGVCIGEKXIVVPHLGYGEGRGNIIPGSAV 354  
DB 304 DSSYSNRNHTYNTYIGQYVTPGMDQGLQACMGERRITIPPHLAYGNGTGDKIPGSAV 363  
QY 355 LVFDIHVIDFHNPSDSISITSHYKPPD-CVLSKKGYLKYHYNASLLDGLTLLDSTWNLG 413  
DB 364 LIPNVHVIDFHNPAVVEIRTLSPSETCNETTKLGDVFRYHYNCSLLDGLTFLTSHDYG 423  
QY 414 KTYNVILGSGQVVLGMDGLREMCVCEKRTVILPPLHGYGAGVGEVPGSAVLVFDIEK 473  
DB 424 APOEATLGANKVIEGLDTGLQCMVGERKQLIVPPHLAHGESGARG-VPGSAVLLEFVEL 482  
QY 474 LELVAGLPEGYMFVWNGEVSPLFEIDKDGNGEVLLBEFSEYIHAQVAGSGKGLAPG 533  
DB 483 VSRDGLPTGYLFWHKKDPPANLFDMDLNDKDGVEPPEEFSTFIKAQVSEKGRMLPQD 542  
QY 534 AELIVKNMFTNQDRNGDKVTAEEFKL---XDOEAKHD 568  
DB 543 PEKTIGDMFQNDQNRQDKITVDELKLSDEDEERVHE 580  
RESULT 4  
AAB12128  
ID AAB12128 standard; Protein; 582 AA.  
XX  
AC AAB12128;  
XX  
DT 02-FEB-2001 (first entry)  
XX

DE Hydrophobic domain protein from clone HPO2991 isolated from KB cells.

KW Human; secreted protein; membrane protein; hydrophobic domain;

KW proliferation control; differentiation induction; material transport;

KW biophysics; signal receptor; ion channel; transporter; immunostimulant;

KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;

KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;

KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

OS Homo sapiens.

XX WO200029448-A2.

PN 25-MAY-2000.

PD 17-NOV-1999; 99WQ-JP06412.

PF 17-NOV-1998; 98JP-0326255.

PR 22-DEC-1998; 98JP-0364315.

PR 16-MAR-1999; 99JP-0069811.

PR 27-APR-1999; 99JP-0119299.

PR 19-MAY-1999; 99JP-0138169.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

PI WPI; 2000-387753/33.

DR N-PSDB; AAA62001, AAA62011.

XX Proteins comprising hydrophobic regions, such as secretory and membrane

XX proteins, useful in research and diagnostics and having various

XX activities e.g. immunomodulatory, antiinflammatory, chemokinetic,

XX hemostatic, thrombolytic -

XX Claim 1; Page 230-232; 410pp; English.

XX Secretory proteins play important roles in the proliferation control, the

XX differentiation induction, the material transport and the biophysics of

XX cells. Membrane proteins have important roles as signal receptors, ion

XX channels and transporters. The present sequence is a human protein which

XX has at least one hydrophobic domain. This protein may be a secretory or a

XX membrane protein. The present protein may have cytokine and cell

XX proliferation/differentiation activity, immune stimulating or suppressing

XX activity, haematopoiesis activity, tissue growth activity,

XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

XX and thrombolytic activity, anti-inflammatory activity and tumour

XX inhibition activity. The present protein could therefore be used for

XX treatment of autoimmune disease, Alzheimer's disease, Parkinson's

XX disease, and cancer.

XX Sequence 582 AA;

Query Match 57.0%; Score 1742; DB 21; Length 582;

Best Local Similarity 56.4%; Pred No. 4.3e-160;

Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;

QY 10 PP-----PLLLLLLWVT-----GQAPVAGLSDAELQIERFVPECPRTVRSQD 55

DB 6 PPSHLLRLFLQLLLLVVQAVGRGLGRASPAGGPLED--VVIERVHIPRACPREVQMGD 63

QY 56 FRYHYVGVTFPDGQKFDSSVDRDSTNFVFGKGLITGMDQALVGMVNERBFRVKTIPPKL 115

DB 64 FRYHYNGTFEDGKFDSSVDRDNTLVAIVGVGRLLITGMDRGLMGVNERRLVPPHL 123

QY 116 AYGNERVGVIPNSVHFDVLMDIWNSEDQVQIHTYFKPSCPRTIQVDFRVHYNG 175

DB 124 GYSGIAGLIPDATALYFDVLLDVNKNEDTVQVSTLLRPHCPRNVDGDFRVHYNG 183

QY 176 TFLDGLTFLDSSSHRMKTYDTYVIGWLIIPGMDKGLMGCVGEKRTITTPETLAYGSDGQ 235

DB 184 TLJDGTSFDTYSKGTDTYVVGSGWLIKMGDGLMGCFGERKRIIPFLAYGKGYG 243

QY 236 KDIPQASLVPDVALLDLHNPCKDISIENKVVPCNERISQSGDLTYHYNGTLDDGTLF 295

DB 244 TVIPQASLVPDVALLDLHNPCKDISIENKVVPCNERISQSGDLTYHYNGTLDDGTLF 303

QY 296 DSSYSRNRFTDYIQGGVYIPGMDGGLGVCIGEKXIVVPPHLYGYGEGRGN-IPGSV 354

DB 304 DSSYSRNRFTDYIQGGVYIPGMDGGLGVCIGEKXIVVPPHLYGYGEGRGN-IPGSV 363

QY 355 LVFDIHWIDFHNPSDSISITSHYKPPD-CSVLKSGDYLYKHYNASLLDGTLLDSTWNLG 413

DB 364 LIFNVHVIDFHNPAVVEIRTLRSPSETCNETTKGLDFVRHYNCSLDGTQLETSHDYG 423

QY 414 KTYNIVLGSQGVWLGMDMGLFREMCMVGEKRTVIIIPPHLYGYGAGVDGVPVGSVAVLFOIE 473

DB 424 APQEATLGANKRVIEGLDTGLQGMVGERQLIVPPLAHGSGARG-VPGSAVLLFEVEL 482

QY 474 LELVAGLPEGVNFTWNGEVSPLFEEDKOGNGEVLLLEEFSEYTHAQVASGKGLAPGFD 533

DB 483 VSREDGLPTGYLFWHKDPPANLFEEDKOGNGEVLLLEEFSEYTHAQVASGKGLAPGFD 542

QY 534 AELIVKQNFNTQDRNGDGKVTAEFKL---XDQEAHCHD 568

DB 543 PEKTIGDMFQNDQNDQKTIIVDELKLSDEDEERVHE 580

RESULT 5

AAV52294

ID AAV52294 standard; Protein; 582 AA.

XX AC AAV52294;

XX DT 09-FEB-2000 (first entry)

XX DE Human isomerase homologue-1 (HIH-1).

XX KW Human isomerase homologue; HIH; FKBP65; PPIase;

XX KW peptidyl-prolyl cis/trans isomerase; FK506; rapamycin;

XX KW signalling pathway; T-cell; cancer; leukaemia; testicular cancer;

XX KW melanoma; immune disorder; asthma; atherosclerosis; diagnosis; treatment;

XX KW prevention; detection; agonist; antagonist; expression; activity;

XX KW antibody; apoptosis; gene therapy; genetic immunisation; vaccine.

XX Homo sapiens.

Key Location/Qualifiers

Region 210..238

/note= "FKBP-type peptidyl-prolyl cis/trans isomerase signature sequence"

Domain 555..567

/note= "EF-hand calcium-binding domain"

Region 579..582

/note= "Endoplasmic reticulum targeting sequence"

Modified-site 70

/note= "N-glycosylated"

Modified-site 72

/note= "Phosphorylated by casein kinase II"

Modified-site 81

/note= "Phosphorylated by casein kinase II"

Modified-site 83

/note= "Phosphorylated by tyrosine kinase"

Modified-site 100

/note= "Phosphorylated by casein kinase II"

Modified-site 182

/note= "N-glycosylated"

Modified-site 184

/note= "Phosphorylated by casein kinase II"

Modified-site 189

/note= "Phosphorylated by casein kinase II"

Modified-site 294

/note= "N-glycosylated"

Modified-site 296

/note= "Phosphorylated by casein kinase II"



FT Modified-site 301 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 310 /note= "N-glycosylated"  
 FT Modified-site 342 /note= "Phosphorylated by cAMP/cGMP-dependent protein kinase"  
 FT Modified-site 352 /note= "N-glycosylated"  
 FT Modified-site 391 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 393 /note= "N-glycosylated"  
 FT Modified-site 395 /note= "Phosphorylated by protein kinase C"  
 FT Modified-site 407 /note= "N-glycosylated"  
 FT Modified-site 409 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 418 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 484 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 546 /note= "Phosphorylated by casein kinase II"  
 FT Modified-site 563 /note= "Phosphorylated by casein kinase II"  
 FT US5989860-A.  
 XX 23-NOV-1999.  
 XX 12-DEC-1997; 97US-0989386.  
 XX 12-DEC-1997; 97US-0989386.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Corley NC, Shah P, Bandman O, Hillman JL, Guegler KJ;  
 XX WPI; 2000-022783/02.  
 XX N-PSDB; AA232925.  
 XX Nucleic acids encoding human isomerase homologs useful for the  
 XX prevention, diagnosis and treatment of cancers and immune disorders -  
 XX Claim 1; Fig 1; 49pp; English.  
 XX This sequence represents human isomerase homologue-1 (HIH-1).  
 CC Nucleotides encoding HIH-1 were first identified in an ovarian tumour  
 CC cDNA library, the cDNA encoding this sequence being a consensus. HIH-1  
 CC is also expressed in other cancerous tissues, lymph nodes, inflamed  
 CC colon, and synovium. HIH-1 has chemical and structural homology with  
 CC mouse FKBP65, sharing 88% identity as well as the isomerase signature  
 CC sequence, the endoplasmic reticulum targeting sequence and many of the  
 CC potential phosphorylation sites. FKBP65 (FK506 binding proteins) are a  
 CC family of peptidyl-prolyl cis/trans isomerases (PPIases) which catalyse  
 CC the cis to trans isomerisation of certain proline imidic bonds in  
 CC proteins. FKBP65 can bind the potent immunosuppressants FK506 and  
 CC rapamycin, inhibiting PPIase activity and thus blocking signalling  
 CC pathways in T-cells. The expression pattern of HIH-1 and its homology  
 CC with FKBP65 indicate that it plays a role in cancers (e.g., leukaemia,  
 CC testicular cancer and melanoma) and immune disorders (e.g., asthma and  
 CC atherosclerosis). HIH proteins, and the nucleotides that encode them, may  
 CC be used for the diagnosis, treatment or prevention of such diseases. HIH  
 CC proteins may be used to identify agonists and antagonists of expression  
 CC and/or activity, and to raise antibodies. The antibodies and antagonists  
 CC may be used to downregulate expression and/or activity and increase  
 CC apoptosis, and the antibodies may also be used in detection of HIH  
 CC proteins and diagnosis of associated diseases. HIH nucleotides may  
 CC be used in gene therapy or in the production of recombinant protein  
 CC either in vitro, or in vivo (e.g., as part of genetic immunisation  
 CC protocol).

XX SQ Sequence 582 AA;  
 Query Match 57.0%; Score 1742; DB 21; Length 582;  
 Best Local Similarity 56.4%; Pred. No. 4.3e-160;  
 Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;  
 Qy 10 PP-----PLLLLLLWT-----GQAPVAGLSGDAELQIERRFVDPDCPRVRSQD 55  
 Db 6 PPSHLLFLPLQLLLLVVQAVRGLGRASPAGGLE--VVIERYHIIPRACPREVQMGD 63  
 Qy 56 FVRHYVCTFPDGOKFSSYDRDSTFNFGKGLITGMDQALVGMCMYNNRFFVKPKL 115  
 Db 64 FVRHYNGTFFDGKFKFSSYDRNTLVAIVGVGRLLITGMDRGLMCMYNNRRLVPPHL 123  
 Qy 116 AYGNERSGVIPPNVSLHFDVLLMDIWNSEDOVQHTVFKPPSCPTTQVDFVRYHYNG 175  
 Db 124 GYGSIGLAGLIPPDATLYFVLLDVNKKEDTVQSTLLRPPHCPRMVQDGFVRYHYNG 183  
 Qy 176 TFLDGTFLDSSHNRMKTYDVTYVIGLIPGMGKGLGCMVGEKRIITPPFLAYGEDGDG 235  
 Db 184 TLLDGTSTFDTYSKGGTYDVTYVGSGLWLGMDQGLGCMVGEKRIITPPFLAYGEKYG 243  
 Qy 236 KDIPQASLVFDVALLDHNPKDSISIEKNVVPENCERISQSGDFLTTHYNGTLLDGTLP 295  
 Db 244 TVIPQASLVFHVLLIDVHNPKDAVQLETLPQGCVRAGAGDFMRVHYNGSLMDGTLP 303  
 Qy 296 DSSYRNRTFTYIGQYVPCMDGELLGVCIGEXXIVVPHLGVGEGRGN-IPGSV 354  
 Db 304 DSSYRNHTYNTYIGQYIIPGMQDGLQACMGERRRITIPPHLAYGENTGDKIPGSV 363  
 Qy 355 LVFDTHVIDFHNPSDSISITSHYKPD-CSVLSKKGDYLYKHYNASLLDGTLLDSTWNLG 413  
 Db 364 LIFNVHVIDFHNPAVDVEIRTLSPSETCNETTKLGDVRYHYNCSLLDGTQLFTSHDYG 423  
 Qy 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTIIPPHLGVGEAGVGEVPGSAVLVFDIEX 473  
 Db 424 APQEATLGANKVIEGLDTGLQCMVGERQLIVPPHLAGESGARG-VFGSAVLLFEVL 482  
 Qy 474 LELVAGLPGYMFPIWNGEVSPLFEIDKNGEVLLEFSEYIHAQVAGSKGLAPGPD 533  
 Db 483 VSREDGLPTGYLFVWHKOPPANLFDMDLNKGGEVPEEFSTFIKAQVSEKGRLLMPGD 542  
 Qy 534 AELIVKNMFTNDRNGDGKVTAEFKL---XDOEAKHD 568  
 Db 543 PEKTIGDMFQNDQNDQDKITVDELKLSDEDEERVHE 580  
 RESULT 6  
 ID AAY23887  
 XX AAY23887 standard; Protein; 388 AA.  
 AC AAY23887;  
 DT 21-SEP-1999 (first entry)  
 XX Amino acid sequence of a FK506 binding protein 65.  
 XX Human; FK506 binding protein; FKBP65; immune system disorder;  
 XX immune cell; hematopoietic cell disorder; thrombolytic activity;  
 XX blood coagulation disorder; blood platelet disorder; wound;  
 XX heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
 XX asthma; allergic asthma; respiratory problem; anaphylaxis;  
 XX hypersensitivity; blood group incompatibility; organ rejection;  
 XX graft versus host disease; inflammatory condition;  
 XX ischemia-reperfusion injury; endotoxin lethality; arthritis;  
 XX complement-mediated hyperacute rejection; nephritis; lung injury;  
 XX inflammatory bowel disease; Crohn's disease; infection.  
 OS Homo sapiens.  
 XX WO9935160-A1.  
 PN  
 XX

PD 15-JUL-1999.  
 XX 06-JAN-1999; 99WO-US00120.  
 PF 09-JAN-1998; 98US-0070875.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 XX Moore PA, Ruben SM, Wei Y;  
 PI WPI; 1999-430382/36.  
 XX N-PSDB; AAX86148.  
 DR New nucleic acids encoding human FK506 binding proteins  
 XX Claim 12; Fig 4; 87pp; English.

CC The present sequence represents a human FK506 binding protein 65  
 CC (FKBP65). It is a splice variant of the sequence given in AAX86147.  
 CC The polypeptide or polynucleotide may be useful in treating deficiencies  
 CC or disorders of the immune system, by activating or inhibiting the  
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune  
 CC cells. They may be useful in treating or detecting deficiencies or  
 CC disorders of hematopoietic cells, to increase differentiation and  
 CC proliferation of hematopoietic cells including the pluripotent stem  
 CC cells, in an effort to treat those disorders associated with a decrease  
 CC in certain types of hematopoietic cells. They can be used to modulate  
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood  
 CC coagulation disorders, blood platelet disorders or wounds resulting from  
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
 CC strokes or scarring. They can also treat autoimmune disorders, allergic  
 CC reactions and conditions such as asthma (particularly allergic asthma)  
 CC or other respiratory problems, anaphylaxis, hypersensitivity to an  
 CC antigenic molecule, or blood group incompatibility, organ rejection or  
 CC graft versus host disease, inflammatory conditions, both chronic and  
 CC acute, including inflammation associated with infection.  
 CC ischaemia-reperfusion injury, endotoxin lethality, arthritis,  
 CC chemokine-induced lung injury, inflammatory bowel disease, or Crohn's  
 CC disease. They can also be used to treat viral, bacterial, fungal and  
 CC parasitic infections.

XX Sequence 388 AA;  
 SQ Query Match 52.6%; Score 1606; DB 20; Length 388;  
 Best Local Similarity 98.1%; Pred. No. 3.8e-147;  
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 195 TVVGIGWLPDGMKGLLGMVCKRITITPPFLAYGEDGDKDIPQASLVDVALLDLH 254  
 DB 1 TYGEIGWLPDGMKGLLGMVCKRITITPPFLAYGEDGDKDIPQASLVDVALLDLH 60  
 QY 255 NPKDSISIKVVPNCERISQSGDFLTYHNGTLLDGLTFSSYRNFTFTYIGQGV 314  
 DB 61 NPKDSISIKVVPNCERISQSGDFLTYHNGTLLDGLTFSSYRNFTFTYIGQGV 120  
 QY 315 IPQMDGLLGVCI GERXIVPPHLYGEGRNIPGSALVFDHIVDFHNPDSISIT 374  
 DB 121 IPQMDGLLGVCI GERXIVPPHLYGEGRNIPGSALVFDHIVDFHNPDSISIT 180  
 QY 375 SHYKPPDCSVLSKKGDLKYHYNASLLDGLTWNLGKTYNVLGSGQVVLGMDMGLR 434  
 DB 181 SHYKPPDCSVLSKKGDLKYHYNASLLDGLTWNLGKTYNVLGSGQVVLGMDMGLR 240  
 QY 435 EMCVGERKTVIIPPHLYGEGAGVDGVPASVAVFDIEXLELVAGLPEGYMTFWNEVSP 494  
 DB 241 EMCVGERKTVIIPPHLYGEGAGVDGVPASVAVFDIEXLELVAGLPEGYMTFWNEVSP 300  
 QY 495 NLFEEIDK 502  
 DB 301 NLFEEINK 308

RESULT 7  
 AAY23885  
 ID AAY23885 standard; Protein; 441 AA.  
 XX AAY23885;  
 AC AAY23885;  
 DT 21-SEP-1999 (first entry)  
 XX Amino acid sequence of a FK506 binding protein 65.  
 DE Human; FK506 binding protein; FKBP65; immune system disorder;  
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
 KW blood coagulation disorder; blood platelet disorder; wound;  
 KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
 KW hypersensitivity; blood group incompatibility; organ rejection;  
 KW graft versus host disease; inflammatory condition;  
 KW ischaemia-reperfusion injury; endotoxin lethality; arthritis;  
 KW complement-mediated hyperacute rejection; nephritis; lung injury;  
 KW inflammatory bowel disease; Crohn's disease; infection.  
 OS Homo sapiens.  
 XX WO9935160-A1.  
 XX 15-JUL-1999.  
 XX 06-JAN-1999; 99WO-US00120.  
 XX 09-JAN-1998; 98US-0070875.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Moore PA, Ruben SM, Wei Y;  
 WPI; 1999-430382/36.  
 N-PSDB; AAX86148.  
 New nucleic acids encoding human FK506 binding proteins  
 Claim 12; Fig 2; 87pp; English.

CC The present sequence represents a human FK506 binding protein 65  
 CC (FKBP65). It is a splice variant of the sequence given in AAX86145.  
 CC The polypeptide or polynucleotide may be useful in treating deficiencies  
 CC or disorders of the immune system, by activating or inhibiting the  
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune  
 CC cells. They may be useful in treating or detecting deficiencies or  
 CC disorders of hematopoietic cells, to increase differentiation and  
 CC proliferation of hematopoietic cells including the pluripotent stem  
 CC cells, in an effort to treat those disorders associated with a decrease  
 CC in certain types of hematopoietic cells. They can be used to modulate  
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood  
 CC coagulation disorders, blood platelet disorders or wounds resulting from  
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
 CC strokes or scarring. They can also treat autoimmune disorders, allergic  
 CC reactions and conditions such as asthma (particularly allergic asthma)  
 CC or other respiratory problems, anaphylaxis, hypersensitivity to an  
 CC antigenic molecule, or blood group incompatibility, organ rejection or  
 CC graft versus host disease, inflammatory conditions, both chronic and  
 CC acute, including inflammation associated with infection.  
 CC ischaemia-reperfusion injury, endotoxin lethality, arthritis,  
 CC chemokine-induced lung injury, inflammatory bowel disease, or Crohn's  
 CC disease. They can also be used to treat viral, bacterial, fungal and  
 CC parasitic infections.

XX Sequence 441 AA;  
 SQ Query Match 45.8%; Score 1399; DB 20; Length 441;  
 Best Local Similarity 58.0%; Pred. No. 6.1e-127;  
 Matches 255; Conservative 77; Mismatches 102; Indels 6; Gaps 4;

QY 134 FDVLLMDIWNSEDQVQIHTYFKPPSCPRITIQVDFVRHYHNGTFLDGTLPDSSNNRMKTY 193  
Db 1 FDVLLDWNKEDTVQVSTLLRPPHCPRMVQDGFVRHYHNGTFLDGTSPDTSYKGGTY 60  
QY 194 DTYVIGIHLIIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDL 253  
Db 61 DTYVSGWLIIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDL 120  
QY 254 HNPXDSISIEKNVVPENCERISQSGDFTYHNGTFLDGTLPDSSNNRMKTY 313  
Db 121 HNPXDAVQLETLPPGCVRRAGAGDFVRHYHNGTFLDGTLPDSSNNRMKTY 180  
QY 314 VIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDL 372  
Db 181 IIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDL 240  
QY 373 ITSHYKPPD-CVSLKSGDYLKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDM 431  
Db 241 IRTLSRPSETCNETTKLGDVFRHYHNGTFLDGTLPDSSNNRMKTY 300  
QY 432 GLRENCVGEKRTVITPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFINWGE 491  
Db 301 GLQGMCMGERRQLIVPPHLAGESGARG-VPGSAVLVFEVLVSREDGLPTGYLFWHKD 359  
QY 492 VSPNLFEEIDKNGEVLLESESEYIHAQVASKGKLAPGDAELIVKMTNDRNGDG 551  
Db 360 PPNLFFEDIDLKNGEVPPEEFSTFIKAQVSEKGRMLPGQPEKTIGMDFQNRDNGQ 419  
QY 552 KYTAEFKL---XDOEAKHD 568  
Db 420 KITVDELKLSDEDEERVHE 432

RESULT 8  
ID AAB54356 standard; Protein; 434 AA.  
XX AAB54356;  
AC AAB54356;  
XX 09-MAR-2001 (first entry)  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:808.  
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
KW detection; diagnosis; identification; cytostatic; neuroprotective;  
KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;  
KW antiinflammatory; cardiac; gene therapy; chromosome mapping;  
KW linkage analysis; tissue identification; tissue typing; forensic;  
KW neural; immune system; muscular; reproductive; gastrointestinal;  
KW pulmonary; cardiovascular; renal; proliferative.  
XX Homo sapiens.  
OS  
XX WO200055320-A1.  
PN  
XX 21-SEP-2000.  
PD  
XX 08-MAR-2000; 2000WO-US05989.  
PF  
XX 12-MAR-1999; 99US-0124270.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2000-579444/54.  
DR  
XX N-PSDB; AAC99121.  
XX  
PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
PT treating, or ameliorating a medical condition, particular pancreatic  
PT cancer, or for use in assays for diagnosing a pathological condition -  
XX  
XX Claim 11; Page 1260-1261; 1379pp; English.

XX AAC98773 to AAC99231 encode the human pancreatic cancer associated  
CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,  
CC gynaecological, cardiac and antiinflammatory activities, and can be used  
CC in gene therapy. The polynucleotide and proteins can be used for  
CC preventing, treating, or ameliorating a medical condition or in assays  
CC for diagnosing a pathological condition or a susceptibility to one in a  
CC subject. Binding partners to the proteins and the activity of the  
CC proteins can be identified. The pancreatic cancer antigens can be used to  
CC detect, treat or prevent pancreatic disorders, especially cancer.  
CC Agonists and antagonists to the antigens can be screened for. The  
CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
CC acid hybridisation probes that can be used in chromosome mapping, linkage  
CC analysis, tissue identification and/or typing and a variety of forensic  
CC and diagnostic methods. The proteins can be used to generate antibodies  
CC which are used to purify, detect and target the polypeptides, including  
CC both in vivo and in vitro diagnostic and therapeutic methods. The  
CC proteins can be used to treat or prevent neural, immune system, muscular,  
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
CC sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 434 AA;  
Query Match 44.3%; Score 1354; DB 21; Length 434;  
Best Local Similarity 57.5%; Pred No. 1.4e-122;  
Matches 249; Conservative 76; Mismatches 102; Indels 6; Gaps 4;  
QY 141 IWNSEDQVQIHTYFKPPSCPRITIQVDFVRHYHNGTFLDGTLPDSSNNRMKTYDTYVIG 200  
Db 1 IRHEEDTVQVSTLLRPPHCPRMVQDGFVRHYHNGTFLDGTSPDTSYKGGTYDTYVIG 60  
QY 201 WLIIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDLNPKDSI 260  
Db 61 WLIIPGMDGLLGMCMGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDLNPKDAV 120  
QY 261 STENKVPENCERISQSGDFTYHNGTFLDGTLPDSSNNRMKTYDTYVIGMD 320  
Db 121 QLETLELPPGCVRRAGAGDFVRHYHNGTFLDGTLPDSSNNRMKTYDTYVIGMDQ 180  
QY 321 GLQGVICGKRIIVPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFINWGE 379  
Db 181 GLQGVICGKRIITIPPELAYGSDGKDIIPGQASLVEDVALLDLNPKDAV 240  
QY 380 PD-CVSLKSGDYLKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDGLREMCV 438  
Db 241 SETCNETTKLGDVFRHYHNGTFLDGTLPDSSNNRMKTYDTYVIGMDQ 300  
QY 439 GEKRTVITPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFINWGEVSPNLF 498  
Db 301 GERRQLIVPPHLAGESGARG-VPGSAVLVFEVLVSREDGLPTGYLFWHKDPPANLFE 359  
QY 499 EIDKNGEVLLESESEYIHAQVASKGKLAPGDAELIVKMTNDRNGDGKVTAEF 558  
Db 360 DMDLNDKGEVPPPEEFSTFIKAQVSEKGRMLPGQPEKTIGMDFQNRDNGD 419  
QY 559 KL---XDOEAKHD 568  
Db 420 KLSDEDEERVHE 432  
RESULT 9  
ID AAB54356 standard; Protein; 166 AA.  
XX AAB54356;  
AC AAB54356;  
XX 23-AUG-2002 (first entry)  
DT Human ovarian antigen HOFMO23, SEQ ID NO:2257.  
XX  
XX



Query Match 24.9%; Score 760; DB 22; Length 1241;  
Best Local Similarity 39.4%; Pred. No. 4e-64;  
Matches 175; Conservative 62; Mismatches 117; Indels 90; Gaps 12;

QY 201 WLI-PQMDKGLGCMVGEKRIITIPFLAYGEDGDKD-----237  
Db 6 WLADQGHGGAAGHVSWEKEIIIPFLAYGEKGYGEGKGHGKFRRRGKNQASTYSCS 65  
QY 238 -----IPQASILFVDAVLLDHNPKDSISIEKVVPPCERISQSGDPL 281  
Db 66 GCILHEGIPRTQGTIVPQASILFVHLIDVHNPKDAVQLETLELPCCVRRAGADPM 125  
QY 282 TYHNGTLDTGLTFSSYGRNRTFYIGQYVIPQMDGGLGVCIQKXIVVPHLY 341  
Db 126 RYHNGSLMDGTLFDSSYGRNHTYTYIGQYIIPQMDGGLGVCIQKXIVVPHLY 185  
QY 342 GREGGN-IPGSAVLVFDTHVDFHNPDSISITSHYKPPD-CSVLKKGDKVLYKHYNAS 399  
Db 186 GENGTDKIPGSAVLVFNHVDVFNHNPADVEIRTSRSECTNCTKGLDFVRYHNC 245  
QY 400 LLDGTLDDSTWNLKTYNIYVLSGQVVLGMDGLREKVCYKXIVVPHLYGEAGVDG 459  
Db 246 LLDGTLQTFSHDYGAQETGANKVIEGLDTGLQCMVGERQLIVPPLAHGESG--G 303  
QY 460 EYVGSVAVLFDIEKLEL-----VAGLPGEYME-----IWN-- 489  
Db 304 VTKIVSVLKYLYAYELHPCIQKNWEEKIPLAKTTLEKTLFWLPHETGRVYLDQAWQAQ 363  
QY 490 --CEVSPNLPFEE---IDKQGNBVL---EEFSEYIHAQVASKGKLAPGDAELIVKXN 541  
Db 364 NYGEKQOQCAEBEGDIEWQLNASVLVQAQEAESLYEDRIITREKDMRVEDPEKVKQW 423  
QY 542 FTNQDRNGDKVTAEBFKLXQDA 565  
Db 424 ----DHSEDEKETDE-----DDEA 438

RESULT 11  
AA57114  
ID AAB57114 standard; Protein; 366 AA.  
XX  
AC AAB57114;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1692.  
XX  
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease.  
XX  
OS Homo sapiens.  
XX  
PN W0200055174-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US05988.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-587513/55.  
XX  
DR N-PSDB; AAF16317.  
XX  
PT Prostate cancer associated gene sequences, referred to as prostate

cancer antigens, useful for treatment, prevention, and diagnosis of  
PT disorders such as prostate cancer -  
XX  
PS Claim 11; Page 2162-2164; 2338pp; English.  
XX  
CC AAF15566 to AAF16505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytoaratic,  
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
CC AAB57303 represent sequences used in the exemplification of the present  
XX invention.  
SQ Sequence 366 AA;  
Query Match 24.3%; Score 743; DB 21; Length 366;  
Best Local Similarity 43.5%; Pred. No. 2.6e-63;  
Matches 165; Conservative 45; Mismatches 91; Indels 78; Gaps 10;

QY 6 WRPP-----PP-----PLLLLLWVT-----GQAPVAGLGS 33  
Db 20 WRLFRSPSPAVPTPTMPFAGPPSHSLRLPLQLLLVQVAGRLGNASGAGPLED 79  
QY 34 AELQIERRFVDPBCPTVRSGDFVRYHYVGTFFDGQKFDSSYDRDSTFNVFVGKQLITG 93  
Db 80 --VVIERYHIPRACPREVQMGDFVRYHNGTPEDKKFDSSYDRNTLVAIVVGVRLITG 137  
QY 94 MDQALVGMCMVNERFVKIPKLAAYGNERSVGVTPPNSVLHFDVLLMDINWSEDOVQHTY 153  
Db 138 MDRGLMGMCMVNERRLIVPHLGYSGTLAGLIPDPAITLFDVLLDWNKEDTVQVSTL 197  
QY 154 FKPPSCPTIOVSDFVRYHYNGTFLDGTLPDSSHNRMTYDVTYVIGWLLPGMDKGLGM 213  
Db 198 LRPHCFRMVQDGDVRYHYNGTLLDGTSTFDSYSGKGTVDYTVGSLWKLKMDQGLGM 257  
QY 214 CVGEKRIITIPFLAYGEDGDKDIPQASILFVDAVLLDLH-----NPKDSISIE 264  
Db 258 CPGERKRIIPFLAYGEKGYGEG--GQG-----HKGFRRRGKNQASTYSCSG 304  
QY 265 KVPENCERISQSGDFLYHYNGTLLDGTFLDSSYSNRRTFDYVIGQY----VIPGMD 320  
Db 305 CILHEGIPRTQGG-----MKSTL-----GATKKGCFGRWWLTLVIPALWE 346  
QY 321 GLLGVCIQKXIVVPPHL 339  
Db 347 AKAGSGRQSIETTVKPL 365

RESULT 12  
AA573884  
ID AAY23884 standard; Protein; 316 AA.  
XX  
AC AAY23884;  
XX  
DT 21-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of FK506 binding protein 65 (FKBP65).  
XX  
KW Human; FK506 binding protein; FKBP65; immune system disorder;  
KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
KW blood coagulation disorder; blood platelet disorder; wound;  
KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
KW hypersensitivity; blood group incompatibility; organ rejection;  
KW graft versus host disease; inflammatory condition;  
KW ischemia-reperfusion injury; endotoxin lethality; arthritis;

KW complement-mediated hyperacute rejection; nephritis; lung injury;  
 XX inflammatory bowel disease; Crohn's disease; infection.  
 OS Homo sapiens.

XX WO9935160-A1.

XX 15-JUL-1999.

XX 06-JAN-1999; 99WO-US00120.

XX 09-JAN-1998; 98US-0070875.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Wei Y;

XX WPI, 1999-430382/36.

XX N-FSDB; AAX86145.

XX New nucleic acids encoding human FK506 binding proteins

XX Claim 12; Fig 1; 87pp; English.

XX The present sequence represents human FK506 binding protein 65 (FKBP65).  
 CC The polypeptide or polynucleotide may be useful in treating deficiencies  
 CC or disorders of the immune system, by activation or inhibiting the  
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune  
 CC cells. They may be useful in treating or detecting deficiencies or  
 CC disorders of hematopoietic cells, to increase differentiation and  
 CC proliferation of hematopoietic cells including the pluripotent stem  
 CC cells, in an effort to treat those disorders associated with a decrease  
 CC in certain types of hematopoietic cells. They can be used to modulate  
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood  
 CC coagulation disorders, blood platelet disorders or wounds resulting from  
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
 CC strokes or scarring. They can also treat autoimmune disorders, allergic  
 CC reactions and conditions such as asthma (particularly allergic asthma) or  
 CC other respiratory problems, anaphylaxis, hypersensitivity to an antigenic  
 CC molecule, or blood group incompatibility, organ rejection or graft versus  
 CC host disease, inflammatory conditions, both chronic and acute, including  
 CC inflammation associated with infection, ischemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,  
 CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel  
 CC disease, or Crohn's disease. They can also be used to treat viral,  
 CC bacterial, fungal and parasitic infections.

XX Sequence 316 AA;

Query Match 24.1%; Score 737; DB 20; Length 316;

Best Local Similarity 58.1%; Pred. No. 8e-63;

Matches 140; Conservative 35; Mismatches 50; Indels 16; Gaps 3;

QY 10 PP-----PLLLLLLVWT-----GOAAPVAGLGSDAELOIERFVDECPRTVRSGD 55

DB 6 PFSHLLRLPLQLLLLVQAVRGGRASAGGPLED--VIERVHIPRACPREVQMGD 63

QY 56 FVRYHYVTFPPDQKFDSSYDRDSTFNVFVGRGQLITGMDQALVGMVNERFVKIPPKL 115

DB 64 FVRYHYNGTFEDGKKFSSYDRNTLVAIVGVGRLITGMDRGLMGVNERRLIVPPHL 123

QY 116 AYGNERSVGIIPNSVLFHFDVLLMDLWNSDOVHTYFKPBPSCPTIOVDFVRHYNG 175

DB 124 GYSGICLAGLIPDATALYFDVLLDWNKEDTVQVSTLLRPHCPRMVQDGFVRHYNG 183

QY 176 TFLDGTLPDSSHNRMTYDYYIGWLIFPMCKGLGCMVGEKRIITIPFFLAYGSDG 235

DB 184 TLLDGTSTFDTYSKGGTYDYYGSGWLKMGDQGLGCMVGEKRIITIPFFLAYGKGYG 243

QY 236 K 236

DB 244 E 244

RESULT 13

AAO05027

XX ID AAO05027 standard; Protein; 127 AA.

XX AC AAO05027;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 18919.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX FN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX DR N-FSDB; AAI84956.

XX Isolated nucleic acids and polypeptides, useful for preventing  
 FT diagnosing and treating e.g. leukaemia, inflammation and immune  
 FT disorders -

XX Claim 20; SEQ ID NO 18919; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 127 AA;

Query Match 21.3%; Score 651; DB 22; Length 127;

Best Local Similarity 97.6%; Pred. No. 4.4e-55;

Matches 123; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 393 SVLSKGGYLYKHYNNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLGMDGLKEMCVGEKR 442

DB 2 SVLSKGGYLYKHYNNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLGMDGLKEMCVGEKR 61

QY 443 TVIIPPHLYGEGAGVDGVPGSVAVLFDIEXLELVAGLPEGYMFVWNGEVSFNLFEEDK 502

DB 62 TVIIPPHLYGEGAGVDGVPGSVAVLFDIEXLELVAGLPEGYMFVWNGEVSFNLFEEDK 121

QY 503 DNGEV 508

DB 122 DNGEV 127

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RESULT 14
AB64697
ID AB64697 standard; Protein; 216 AA.
XX
AC AB64697;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 20883.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
N-PSDB; ABL08800.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 20883; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 216 AA;

Query Match 10.1%; Score 309; DB 22; Length 216;
Best Local Similarity 23.8%; Pred. No. 1.8e-21;
Matches 83; Conservative 50; Mismatches 58; Indels 158; Gaps 8;

QY 241 QASLVPFVALDLHNPXDSISIKV-----PENCERISQSGDFLTYHNGT 288
DB 3 KSNLVISCLL-----VAISNSLRAQDLKVEVISTPEVCQKSKNGDSLTMHYGT 54

QY 289 L-LDGTFLDSSYSNRRTFDYVIGQYVPGMDGLGVCIGEKRXIVVPPHLGYGEEGRG 347
DB 55 LQADKKFDSFDDQFTQLGAGQVTKGWDQGLLNCVCEKRLIIPQLGYDQDQAG 114

QY 348 NPGSAVLVFDHVIDFHNPSDSISITSHYKPPDCSVLSKKGDYLYKHYNASLLDGLLD 407
DB 115 NV----- 116

QY 408 STWNLKTYNVLGSGQVVLGMDMLRCMVCGEKRTVIIPHLGYGEAGVDGVPGSVIL 467
DB 117 -----IppKATL 123

QY 468 VFDIEXLELVAGLPFGYFIWNGEVSFNLFEIDKNGNEVLLEFSEYIHAQVASKGK 527
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Db 124 LFDVELIN-----IGNAPTTNVFKEIDNADKQLSREVSSEYLLKKQMTAVEGO 172
QY 528 -----LAFGFDABELIVKXMTNQDRNGDGKVTAEBFKLDQAKHD 568
DB 173 DSEELKNMLA---ENDKLVEEIFQHEDKXNGFTSHDEF-----SGPKHD 214

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RESULT 15
AAU87239
ID AAU87239 standard; Protein; 131 AA.
XX
AC AAU87239;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #149.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 22-AUG-2000; 2000US-0227182.
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PR 30-AUG-2000; 2000US-0228924.
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| PR | 02-OCT-2000; | 2000US-0236800. |
| PR | 02-OCT-2000; | 2000US-0237037. |
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| PR | 02-OCT-2000; | 2000US-0237040. |
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| PR | 13-OCT-2000; | 2000US-0239937. |
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| PR | 17-NOV-2000; | 2000US-0249211. |
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| PR | 05-DEC-2000; | 2000US-0251988. |
| PR | 05-DEC-2000; | 2000US-0256179. |
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| PR | 05-JAN-2001; | 2001US-0259678. |

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Qy 506 GEVLEEFSEYIHAQVASKGKGLAPGFDALFVKNMFTNQDRNGDGKVTABEFKL---XD 562  
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Qy 563 QEAKHD 568  
Db 124 EERVHE 129

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Job time : 42.2691 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 14.5233 Seconds  
(without alignments)  
1162.874 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 1742   | 57.0  | 582    | 2  | US-08-989-386-1  |
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| 7          | 231.5  | 7.6   | 141    | 2  | US-08-803-899-6  |
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| 25         | 207    | 6.8   | 107    | 4  | US-09-398-193-79 |
| 26         | 207    | 6.8   | 113    | 5  | PCT-US92-03993-4 |
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ALIGNMENTS

RESULT 1  
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; Patent No. 5989860  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,386  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0443 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: amino acid  
; LENGTH: 581 amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 894162  
US-08-989-386-7

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVAR2UT01
; CLONE: 2255114
; US-08-989-386-1

Query Match          57.0%; Score 1742; DB 2; Length 582;
Best Local Similarity 56.4%; Pred. No. 1.2e-166;
Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps

QY 10 PP-----PLLLLLLWVT-----GQAAPVAGLGSDAEQLQIERFVDPCEPRTVRSGD 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 PPSHSLLRLPLQLLLLLLVVQAVRGLGRASPAGGPLED--VVIERYHIPRACPREVQMGD 63

QY 56 FVRVYHVGTFPDGQKFDSSYDRDSTFNFVCGKQLITGMDQALVGMVCYNERRFVKI PPKL 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 FVRVYHNGTFEDCKKFDSSYDRNTLVAIVVUGVRLITGMDRGLMGCMCNERRLVPPHL 123

QY 116 AYGNERSVGVPPNSVLHFDVLLMDIWNSEDQVHTYFKPPSCPRITQVDFVRYHYNG 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 GYGSIGSLAGLIPDADTLFVDVLLDMWNKEDTVQSTLLRPPHPCPRMVQDGFVRYHYNG 183

QY 176 TELDGTFLPSSHNRKMTYDTYVGIGWLIPGMDKGLLGMCMVGEKRIITIPPFILAYGEDGDG 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TLLDGTSPDTSYKSGTYDTYVGSGLIKGMDQGLLGMCPGERRKLIIPPFILAYGEKGVG 243

QY 236 KDI PQASLVPFDVALLDHNPKDSISIKNVVPENCERISQSGDPLTHYNGTLTLDGTLF 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TVIP PQASLVFHVLLIDVHNPKDAVQLETLELPQCVRRAGAGDFMRVHYNGSLMDGTFLF 303

QY 296 DSSYSRNRFTDYICQGVVPGMDGSLGVCITIGEXRXIIVPPHLGYBEGRN-IPGSVA 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 DSSYSRNTYNTYICGVYIIPGMDQGLQACGGERRITIPHLAYGNGTGDKIPGSNAV 363

QY 355 LVFDIIVDFHNPSSISITSHYKPPD-CSVL SKGVDYLNKHYNASLLDGTLLDWTNLG 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 LIFNVHVIDFHNPAVDVIRTLRSRSETCNFTKLGDFVRVHYNCSLLDGTQLFTSHDYG 423

QY 414 KTYNTVLGSGQVVLGMDGLRMCVGEKRTYIIPHLGYGAGVDGVEPGSAVLVFDIEX 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 A PQEATLGANKVIEGLDTGLQMGCGERRQLIVPHLAHGESGARG-VPGSAVLLEFVEL 482

QY 474 LELVAGLPEGYWFIWNGEVS PNLPEIIDKONGEVLLEEFPSYIIHAOVASGKGKLAPOPD 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 VSREPDGLFTGYLVFWHKDPANLFDMDLKNKDGVEYPPPEEFTFIKAOVSEGKRLMPQOD 542

QY 534 ASLIVKNMFTNDRNGDGKVTAEFEKL---XDOEAKHD 568
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 543 PEKTIGDMFQNDNRMDGKIITVDELKLSDEDEERVHE 580
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-08-336-618-20
; Sequence 20, Application US/08336618
; Patent No. 5763590
; *GENERAL INFORMATION:
; APPLICANT: Peattie, Debra A.

```

APPLICANT: Harding, Matthew W.  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING  
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN  
TITLE OF INVENTION: CDNA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,618  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/963,325  
FILING DATE: 16-OCT-1992  
APPLICATION NUMBER: US 07/777,752  
FILING DATE: 11-OCT-1991  
PRIOR APPLICATION DATA: PCT/  
APPLICATION NUMBER: 09-OCT-1992  
FILING DATE: 09-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: VP191-06A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-9240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-618-20

Query Match 8.0%; Score 244.5; DB 1; Length 135;  
Best Local Similarity 43.3%; Pred. No. 7.4e-17;  
Matches 55; Conservative 21; Mismatches 50; Indels 1; Gaps 1;  
QY 16 LLLWVTGQAPVAGLSGDAELQIERRFVDPDCPTVRSGDFVRHYVGT-FPDGQKPDSS 74  
DB 5 IYLFVTFSTILAGSLSDLEIGIKRIPVEDCLIKAMPDGKVKHYTGSLLSGTVDSS 64  
QY 75 YDRSTFNVFVGKQLITGMDQALVGMVNRFRFKIPPKLAYGNRVSGVIPPNSVLHF 134  
DB 65 YSRGSPTAFELGVGRVIKWDQGVAGMVGCKRKLQIPSSLAYGRGVGVIPPSADLVF 124  
QY 135 DVLMDI 141  
DB 125 DVELVDV 131  
RESULT 4  
US-07-822-966B-6  
Sequence 6, Application US/07822966B  
Patent No. 5498597  
GENERAL INFORMATION:  
APPLICANT: Steven J. Burakoff  
APPLICANT: Stuart L. Schreiber  
APPLICANT: Barbara E. Bierer  
TITLE OF INVENTION: FKBP-13, AN FK506-BINDING  
TITLE OF INVENTION: IMMUNOPHILIN  
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/822,966B  
FILING DATE: January 17, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00530/052001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 141 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-822-966B-6  
Query Match 7.9%; Score 242.5; DB 1; Length 141;  
Best Local Similarity 47.7%; Pred. No. 1.3e-16;  
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;  
QY 257 KDSISIKNVKVPENCERISQSGDFLTYYHNGTLLDGTFLDSSYSRNRFTDTYIGQGVIP 316  
DB 29 KLIQGVKKRV--DHCPIKSRKGDVLMHYTKLEDGTEDFSSLPQNPQPFVFSIGTGQVIK 86  
QY 317 GMDEGLLVGICGKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362  
DB 87 GWDQGLMGCEGKRLVPSLGYGEGRAPPKIPGCGATLVFEVLL 133  
RESULT 5  
US-08-336-618-18  
Sequence 18, Application US/08336618  
Patent No. 5763590  
GENERAL INFORMATION:  
APPLICANT: Peattie, Debra A.  
APPLICANT: Harding, Matthew W.  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING  
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN  
TITLE OF INVENTION: CDNA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,618  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-06A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-618-18

Query Match      7.9%; Score 242.5; DB 1; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 30 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTGTFDSSLPQNPQPFVSLGTGVK 87
QY 317 GMDEGLLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362
Db 88 GWDQGLGMCGEKRLVIPSELGYGERGAPPKIPGGATLVFEVLL 134

RESULT 6
PCT-US92-03993-7
; Sequence 7, Application PC/TUS9203993
; GENERAL INFORMATION:
; APPLICANT: Harding, Matthew W.
; TITLE OF INVENTION: RFEP: A NOVEL PROLYL ISOMERASE AND
; TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US92/03993
; FILING DATE: 19920507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/697,113
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-05A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids

```

```

; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-03993-7

Query Match      7.9%; Score 242.5; DB 5; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 30 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTGTFDSSLPQNPQPFVSLGTGVK 87
QY 317 GMDEGLLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362
Db 88 GWDQGLGMCGEKRLVIPSELGYGERGAPPKIPGGATLVFEVLL 134

RESULT 7
US-08-803-899-6
; Sequence 6, Application US/08803899
; Patent No. 5912224
; GENERAL INFORMATION:
; APPLICANT: DONAHUE, PATRICIA K.
; APPLICANT: WANG, TONGWEN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,899
; FILING DATE: 02/21/1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/012,054
; FILING DATE: 02/22/1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609,4240001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-803-899-6

Query Match      7.6%; Score 231.5; DB 2; Length 141;
Best Local Similarity 46.7%; Pred. No. 1.6e-15;
Matches 50; Conservative 17; Mismatches 37; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 29 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTGTFDSSLPQNPQPFVSLGTGVK 86
QY 317 GMDEGLLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362

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```
DB      | :|||: ||| ::|| |||| |   |||:: ::  
87     GWDQGLLGMVEGERKRLVIPSELGYGRCAPPKIPGGATLVFEVLL 133
```

## RESULT 8

US-08-894-173-69  
; Sequence 69, Application US/08894173A

; Patent No. 6090612  
: GENERAL INFORMATION:

Query Match 7.5%; Score 230.5; DB 3; Length 107;  
Best Local Similarity 45.0%; Pred. No. 1.3e-15;  
Matches 50: Conservative 14; Mismatches 42; Indels 5

|    |    |   |    |
|----|----|---|----|
| Qy | 31 | GSDAELQIERRFVDPCEPRTVRSGDFVRHYVGTGTPDQKEDSSYDRDSTFNVFVGKGL  | 90 |
| Dp | 1  | GLQIHEVOOE-----GQCTRETRGDNVDVHYKGVLTSGKKEDASYDRGEPLNFTVGQGV | 55 |

QY 91 ITGMDQALVGMVCVNERPFVKIPPKLAYGNERSVGIIPNSVLHFDVLMDI 141  
 56 IKWDEGIIGMKIGEXBKTIAPHIAYGNRAVGGIIPANSTIJFETELVGI 106  
 Db

## RESULT 9

US-08-894-173-83  
; Sequence 83, Application US/08894173A

; Patent No. 6090612  
: GENERAL INFORMATION:

|                       |        |                    |       |                |
|-----------------------|--------|--------------------|-------|----------------|
| Query Match           | 7.5%;  | Score 230.5;       | DB 3; | Length 107;    |
| Best Local Similarity | 45.0%; | Pred. No. 1.3e-15; |       |                |
| Matches               | 50.    | Conservative       | 14.   | Mismatches 42. |
|                       |        |                    |       | Indels 5       |

QY 31 GSDAEIQIERRFVPDECPRTVRSGDFVHYHVTGTFDPDQKFDSSYDRDSTFNFVCKGQL 90

QY 91 ITGMDQALVGMVCVNERRFVKIPPKLAYGNERVSGVIPPNSSVLHFDVLLMDI 141

Dh 56 TKGWDEGLGAMKIGEKPKTITAPHIAYGNRAVGCIIPANSSTITFEFEIVLGI 106

## RESULT, T 10

RESULT TO  
US-09-398-193-69  
: Sequence 69. Application US/09398193

; sequence 09, Applica  
 ; Patent No. 6197581  
 : GENERAL INFORMATION:

Query Match 7.5%; Score 230.5; DB 4; Length 107;  
Best Local Similarity 45.0%; Pred. No. 1.3e-15;  
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;

Qy 31 GSDAELQIERRFVDECPRTVRSQDFVRYHYVGTFFDQKQFDSSYDRDSTFNVFVGKQL 90

Dh 1 GLOTEVOR-----GCGTFRFRRCNVVDVHYKGVITSGKKFDDASVDRGEPINFTVGGOV 55

QY 91 ITGMDQALVGMCVNERRFVKIPPKLAYGNERSVGVI PPNSVLHFDVLLMDI 141  
| | | | | : | | : | | | | | | | | : | | : |  
Db 56 TKGWDEGLCMKTGEKPKTIAPHIAYGNRAVGGITPANSTLJFETELVGI 106

RESIT, T 11

RESULTS II  
US-09-398-193-83  
; Sequence 83, Application US/09398193

; Patent No. 6197581  
; GENERAL INFORMATION:

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 7.5%             | Score 230.5;       | DB 4;      | Length 107; |
| Best Local Similarity | 45.0%;           | Pred. No. 1.3e-15; |            |             |
| Matches               | 50: Conservative | 14: Mismatches     | 42: Indels | 5: Gaps     |

|    |    |               |         |          |        |          |          |         |          |    |
|----|----|---------------|---------|----------|--------|----------|----------|---------|----------|----|
| QY | 31 | GSDAELQIERRFV | DECPRTV | SGDFVR   | VHYVGT | PDQK     | EDSSYDR  | DSTFN   | VFKGQL   | 90 |
|    |    | :   :         | :       |          |        | :        | :        | :       |          |    |
| dh | 1  | GIOTFVOOE     | -----   | GOSTRETR | GDNDV  | VHYKGVLT | SGKKEDAS | YORGEPL | NFTVGOGV | 55 |

QY 91 ITGMDQALVGMCVNERFVKIPPKLAYGNERSVGVI PPNSVLHFDVLLMDI 141  
| | : | : | : | : | : | : | : | : | : | : | : | : | :  
pb 56 TKCNDEGLCGMKIGRVPKTIADPTAYGNBAVGCIIPANSTLFEETELVGI 106

RESIT.T 12

RESULT 12  
PCT-US92-03993-1  
; Sequence 1, Application PC/TUS9203993

; APPLICANT: Harding, Matthew W.  
; TITLE OF INVENTION: RFXBP: A NOVEL PROLYL ISOMERASE AND  
; TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive

STATE: MA  
COUNTRY: USA  
ZIP: 02173

```

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;

```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03993  
FILING DATE: 19920507  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/697,113  
FILING DATE: 08-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: VPI91-05A PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-03993-1

Query Match 7.5%; Score 230.5; DB 5; Length 119;  
Best Local Similarity 45.0%; Pred. No. 1.6e-15;  
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;  
  
Qy 31 GSDAELQIERRFVDECPRTVRSQDFVRYHYVGTTPDQKFDSSYDRDSTFNFFVGKQL 90  
Db 7 GLQIEVQOE-----GQGTRETRRGDNVDVHYKGLTSGKFDASYDRGEPLNFTVGQGV 61  
Qy 91 ITGMDQALVGMVNERFVKIPPKLAYGNRVSVPNSVLHFDVLLMDI 141  
Db 62 IKGWDGLGKMGKIKERKLTIAPLAYGNRAVGGIIPANSTLIFETELVGI 112

RESULT 13  
US-08-336-618-17  
Sequence 17, Application US/08336618  
Patent No. 5763590  
GENERAL INFORMATION:  
APPLICANT: Peattie, Debra A.  
APPLICANT: Harding, Matthew W.  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING  
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith and Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,618  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/963,325  
FILING DATE: 16-OCT-1992  
APPLICATION NUMBER: US 07/777,752  
FILING DATE: 11-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/  
FILING DATE: 09-OCT-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: VPI91-06A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-618-17

Query Match 7.5%; Score 230.5; DB 1; Length 120;  
Best Local Similarity 45.0%; Pred. No. 1.6e-15;  
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;  
  
Qy 31 GSDAELQIERRFVDECPRTVRSQDFVRYHYVGTTPDQKFDSSYDRDSTFNFFVGKQL 90  
Db 8 GLQIEVQOE-----GQGTRETRRGDNVDVHYKGLTSGKFDASYDRGEPLNFTVGQGV 62  
Qy 91 ITGMDQALVGMVNERFVKIPPKLAYGNRVSVPNSVLHFDVLLMDI 141  
Db 63 IKGWDGLGKMGKIKERKLTIAPLAYGNRAVGGIIPANSTLIFETELVGI 113

RESULT 14  
US-08-894-173-86  
Sequence 86, Application US/08894173A  
Patent No. 6090612  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
TITLE OF INVENTION: Adenylate cyclase and uses therefor  
FILE REFERENCE: P14716C  
CURRENT APPLICATION NUMBER: US/08/894,173A  
CURRENT FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 86  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Yeast  
US-08-894-173-86

Query Match 7.5%; Score 230; DB 3; Length 104;  
Best Local Similarity 46.9%; Pred. No. 1.4e-15;  
Matches 45; Conservative 16; Mismatches 35; Indels 0; Gaps 0;  
  
Qy 381 DCSVLSKKGYLKYHYNASLLDGLDSTWNLGKTYNTVLGSGQVVLGMDGLREMCVGE 440  
Db 8 DCLIKAMPGDKVKVHYTGSLESTGVFDSSYSYSGSPAPAEFGVGRVKGWDQGVAGMCVGE 67  
Qy 441 KRTVIIPHLGYGEAGVDGVEPGSAVLVDFDIELEL 476  
Db 68 KRLQIFSSLAYGERGVGVIPPSADLVDFDELVDV 103

RESULT 15  
US-09-398-193-86  
Sequence 86, Application US/09398193  
Patent No. 6197581  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
TITLE OF INVENTION: Adenylate cyclase and uses therefor  
FILE REFERENCE: P24360-  
CURRENT APPLICATION NUMBER: US/09/398,193  
CURRENT FILING DATE: 1999-09-17  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 86  
LENGTH: 104

; TYPE: PRT  
 ; ORGANISM: Yeast  
 US-09-398-193-86

|    | Query Match           | 7.5%  | Score 230         | DB 4     | Length 104 |
|----|-----------------------|---|-------------------|----------|------------|
|    | Best Local Similarity | 46.9%   | Pred. No. 1.4e-15 |          |            |
|    | Matches 45            | Conservative 16   | Mismatches 35     | Indels 0 | Gaps 0     |
| QY | 381                   | DCSVLSKGGDYLVKHYNASTLLDGTLLDSTNNLKTNYIVLGGGVIVLGMDMGLREMCVGE  | 440               |          |            |
| Db | 8                     | DCLIKAMPGDVKVKVHYTGSLESTGVFVDSRSRGSFIAPELGVGRVIRKWDQGVAGMCVGE | 67                |          |            |
| QY | 441                   | KRTVIIIPHLGYGAGVDGEVPGSAVLVDFDIEXLEL                          | 476               |          |            |
| Db | 68                    | KRKIQIIPSSLIAYGSRGVPGVIPPSSADLVDFVDV                          | 103               |          |            |

Search completed: April 26, 2003, 06:49:51  
Job time : 15.7733 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:51:02 ; Search time 18.1541 Seconds  
(without alignments)  
2533.559 Million cell updates/sec

Title: US-09-225-502-6  
Perfect score: 3054  
Sequence: 1 MAFRGMWRPPPPPLLLLLLW.....AEEFKLXQBAKHDTVTLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCT08\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 3048  | 99.8        | 574    | US-09-225-502-6    | Sequence 6, Appli  |
| 2          | 1606  | 52.6        | 388    | US-09-225-502-8    | Sequence 8, Appli  |
| 3          | 1399  | 45.8        | 441    | US-09-225-502-4    | Sequence 4, Appli  |
| 4          | 1354  | 44.3        | 434    | US-09-925-297-808  | Sequence 808, App  |
| 5          | 743   | 24.3        | 366    | US-09-925-300-1692 | Sequence 1692, App |
| 6          | 737   | 24.1        | 336    | US-09-225-502-2    | Sequence 2, Appli  |
| 7          | 268   | 8.8         | 222    | US-10-006-856A-180 | Sequence 180, App  |
| 8          | 268   | 8.8         | 222    | US-10-006-818A-180 | Sequence 180, App  |
| 9          | 268   | 8.8         | 222    | US-10-015-393A-180 | Sequence 180, App  |
| 10         | 268   | 8.8         | 222    | US-09-946-374-180  | Sequence 180, App  |
| 11         | 268   | 8.8         | 222    | US-10-012-121A-180 | Sequence 180, App  |
| 12         | 268   | 8.8         | 222    | US-10-015-869A-180 | Sequence 180, App  |
| 13         | 256   | 8.4         | 211    | US-09-978-295A-145 | Sequence 145, App  |
| 14         | 256   | 8.4         | 211    | US-09-978-697-145  | Sequence 145, App  |
| 15         | 256   | 8.4         | 211    | US-09-978-192A-145 | Sequence 145, App  |
| 16         | 256   | 8.4         | 211    | US-09-999-832A-145 | Sequence 145, App  |
| 17         | 256   | 8.4         | 211    | US-10-001-054-4    | Sequence 4, Appli  |
| 18         | 256   | 8.4         | 211    | US-09-978-189-145  | Sequence 145, App  |
| 19         | 256   | 8.4         | 211    | US-10-028-072-384  | Sequence 384, App  |

|    |     |     |     |   |                    |                   |
|----|-----|-----|-----|---|--------------------|-------------------|
| 20 | 256 | 8.4 | 211 | 9 | US-10-121-049-384  | Sequence 384, App |
| 21 | 256 | 8.4 | 211 | 9 | US-10-123-904-384  | Sequence 384, App |
| 22 | 256 | 8.4 | 211 | 9 | US-10-140-470-384  | Sequence 384, App |
| 23 | 256 | 8.4 | 211 | 9 | US-10-175-746-384  | Sequence 384, App |
| 24 | 256 | 8.4 | 211 | 9 | US-10-176-918-384  | Sequence 384, App |
| 25 | 256 | 8.4 | 211 | 9 | US-10-176-921-384  | Sequence 384, App |
| 26 | 256 | 8.4 | 211 | 9 | US-10-137-865-384  | Sequence 384, App |
| 27 | 256 | 8.4 | 211 | 9 | US-10-140-474-384  | Sequence 384, App |
| 28 | 256 | 8.4 | 211 | 9 | US-10-142-431-384  | Sequence 384, App |
| 29 | 256 | 8.4 | 211 | 9 | US-10-143-114-384  | Sequence 384, App |
| 30 | 256 | 8.4 | 211 | 9 | US-10-140-002-384  | Sequence 384, App |
| 31 | 256 | 8.4 | 211 | 9 | US-09-978-608A-145 | Sequence 145, App |
| 32 | 256 | 8.4 | 211 | 9 | US-10-142-419-384  | Sequence 384, App |
| 33 | 256 | 8.4 | 211 | 9 | US-09-978-724A-189 | Sequence 189, App |
| 34 | 256 | 8.4 | 211 | 9 | US-09-978-191A-145 | Sequence 145, App |
| 35 | 256 | 8.4 | 211 | 9 | US-09-978-403A-145 | Sequence 145, App |
| 36 | 256 | 8.4 | 211 | 9 | US-09-978-564A-145 | Sequence 145, App |
| 37 | 256 | 8.4 | 211 | 9 | US-09-978-585A-145 | Sequence 145, App |
| 38 | 256 | 8.4 | 211 | 9 | US-10-017-081A-145 | Sequence 145, App |
| 39 | 256 | 8.4 | 211 | 9 | US-10-123-262-384  | Sequence 384, App |
| 40 | 256 | 8.4 | 211 | 9 | US-10-142-423-384  | Sequence 384, App |
| 41 | 256 | 8.4 | 211 | 9 | US-09-978-824-145  | Sequence 145, App |
| 42 | 256 | 8.4 | 211 | 9 | US-09-981-915A-145 | Sequence 145, App |
| 43 | 256 | 8.4 | 211 | 9 | US-09-999-833A-145 | Sequence 145, App |
| 44 | 256 | 8.4 | 211 | 9 | US-10-121-050-384  | Sequence 384, App |
| 45 | 256 | 8.4 | 211 | 9 | US-10-141-755-384  | Sequence 384, App |

ALIGNMENTS

RESULT 1

US-09-225-502-6  
; Sequence 6, Application US/09225502A  
; Patent No. US20020137127A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore et al.  
; TITLE OF INVENTION: Human FK506 Binding Proteins  
; FILE REFERENCE: PF392  
; CURRENT APPLICATION NUMBER: US/09/225,502A  
; CURRENT FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/070,875  
; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-225-502-6

Query Match 99.8%; Score 3048; DB 10; Length 574;  
Best Local Similarity 100.0%; Pred. No. 4.4e-259;  
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MAFRGMWRPPPPPLLLLLLWVTGQAAPVAGLGSDAELQIERRFVDPDECPTVRSGDFVRYH | 60  |
| DB | 1   | MAFRGMWRPPPPPLLLLLLWVTGQAAPVAGLGSDAELQIERRFVDPDECPTVRSGDFVRYH | 60  |
| QY | 61  | YVGTFFDQGFDSYDSDSTFNVFGKQLITGMDQALVGMVNERFVKIPPKLAYGNE        | 120 |
| DB | 61  | YVGTFFDQGFDSYDSDSTFNVFGKQLITGMDQALVGMVNERFVKIPPKLAYGNE        | 120 |
| QY | 121 | RVSQVIPPNSVLPHFDVLLMDIWNSEDQVQHTYFKPSPCRPTIQVSDFVRHYNGTFLDG   | 180 |
| DB | 121 | RVSQVIPPNSVLPHFDVLLMDIWNSEDQVQHTYFKPSPCRPTIQVSDFVRHYNGTFLDG   | 180 |
| QY | 181 | TLFDSSHNRMKTYTYVIGIWLIPGMDKLLGCMVGKRIITIPPLAYGDEGDKDIPG       | 240 |
| DB | 181 | TLFDSSHNRMKTYTYVIGIWLIPGMDKLLGCMVGKRIITIPPLAYGDEGDKDIPG       | 240 |
| QY | 241 | QASLAFVDVALLDHNPKDSTSIENKVPENCERISQSGDFTYHYNGTFLDGTLPDSSYS    | 300 |

Db 241 QASLVFDVALLDLHNPCKDSISIKNVVPCNCERISQSGDFLTYYHNGTLLDGLTLPDSSYS 300  
 Qy 301 RNRFTPTIYGQGVIPGMDGGLGVCIGKRXIIVPPHLYGEGRGNIIPGSAVLVFDIHL 360  
 Db 301 RNRFTPTIYGQGVIPGMDGGLGVCIGKRXIIVPPHLYGEGRGNIIPGSAVLVFDIHL 360  
 Qy 361 VIDFNPDSISITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVL 420  
 Db 361 VIDFNPDSISITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVL 420  
 Qy 421 GSGQVVLGMDGLRENCVCGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGL 480  
 Db 421 GSGQVVLGMDGLRENCVCGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGL 480  
 Qy 481 PEGYMFVWGEVSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVN 540  
 Db 481 PEGYMFVWGEVSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVN 540  
 Qy 541 MFTNQRNGDKVTAEEFKLXQDAKHDTNLIA 574  
 Db 541 MFTNQRNGDKVTAEEFKLXQDAKHDTNLIA 574

## RESULT 2

US-09-225-502-8  
 ; Sequence 8, Application US/09225502A  
 ; Patent No. US20020137127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Moore et al.  
 ; TITLE OF INVENTION: Human FK506 Binding Proteins  
 ; FILE REFERENCE: PF392  
 ; CURRENT APPLICATION NUMBER: US/09/225,502A  
 ; CURRENT FILING DATE: 1999-01-06  
 ; PRIOR APPLICATION NUMBER: 60/070,875  
 ; PRIOR FILING DATE: 1998-01-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 388  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-225-502-8

Query Match 52.6%; Score 1606; DB 10; Length 388;  
 Best Local Similarity 98.1%; Pred. No. 8.3e-133;  
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 195 TVYIGWLIPGMDKGLGKVCGERKTIIPPHLYGEGAGVDPGSAVLVFDVALLDLH 254  
 Db 1 TYGEIGWLIPGMDKGLGKVCGERKTIIPPHLYGEGAGVDPGSAVLVFDVALLDLH 60  
 Qy 255 NPKDSISIKNVVPCNCERISQSGDFLTYYHNGTLLDGLTLPDSSYSNRRTFTDIYIGQYV 314  
 Db 61 NPKDSISIKNVVPCNCERISQSGDFLTYYHNGTLLDGLTLPDSSYSNRRTFTDIYIGQYV 120  
 Qy 315 IPGMDGGLGVCIGKRXIIVPPHLYGEGAGVDPGSAVLVFDIHDVFNHPSISIT 374  
 Db 121 IPGMDGGLGVCIGKRXIIVPPHLYGEGAGVDPGSAVLVFDIHDVFNHPSISIT 180  
 Qy 375 SHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMDMGLR 434  
 Db 181 SHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240  
 Qy 435 EMCVGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFVWGEVSP 494  
 Db 241 EMCVGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFVWGEVSP 300  
 Qy 495 NLFEEDK 502  
 Db 301 NLFEEDK 308

## RESULT 3

US-09-225-502-4  
 ; Sequence 4, Application US/09225502A  
 ; Patent No. US20020137127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Moore et al.  
 ; TITLE OF INVENTION: Human FK506 Binding Proteins  
 ; FILE REFERENCE: PF392  
 ; CURRENT APPLICATION NUMBER: US/09/225,502A  
 ; CURRENT FILING DATE: 1999-01-06  
 ; PRIOR APPLICATION NUMBER: 60/070,875  
 ; PRIOR FILING DATE: 1998-01-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 441  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-225-502-4

Query Match 45.8%; Score 1399; DB 10; Length 441;  
 Best Local Similarity 58.0%; Pred. No. 1.4e-114;  
 Matches 255; Conservative 77; Mismatches 102; Indels 6; Gaps 4;

Qy 134 FVLLMDIWNSEDQVQIHTYFKPDPSCPTIQVDFVRYHNGTLLDGLTLPDSSHNMKTY 193  
 Db\* 1 FVLLMDIWNSEDQVQIHTYFKPDPSCPTIQVDFVRYHNGTLLDGLTLPDSSHNMKTY 193  
 Qy 194 DTYVIGWLIPGMDKGLGKVCGERKTIIPPHLYGEGAGVDPGSAVLVFDVALLDL 253  
 Db 61 DTYVIGWLIPGMDKGLGKVCGERKTIIPPHLYGEGAGVDPGSAVLVFDVALLDL 120  
 Qy 254 HNPCKDSISIKNVVPCNCERISQSGDFLTYYHNGTLLDGLTLPDSSYSNRRTFTDIYIGQY 313  
 Db 121 HNPCKDSISIKNVVPCNCERISQSGDFLTYYHNGTLLDGLTLPDSSYSNRRTFTDIYIGQY 180  
 Qy 314 VIPGMDGGLGVCIGKRXIIVPPHLYGEGAGVDPGSAVLVFDIHDVFNHPSISIT 372  
 Db 181 VIPGMDGGLGVCIGKRXIIVPPHLYGEGAGVDPGSAVLVFDIHDVFNHPSISIT 240  
 Qy 373 ITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMDM 431  
 Db 241 ITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMDM 300  
 Qy 432 GLRENCVCGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFVWGEVSP 491  
 Db 301 GLRENCVCGERKTIIPPHLYGEGAGVDPGSAVLVFDIEXLELVAGLPEGYMFVWGEVSP 359  
 Qy 492 VSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVNMTNQRNGDG 551  
 Db 360 VSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVNMTNQRNGDG 419  
 Qy 552 KVTAEEFKLXQDAKHDTNLIA 574  
 Db 420 KVTAEEFKLXQDAKHDTNLIA 439

## RESULT 4

US-09-225-297-808  
 ; Sequence 808, Application US/09925297  
 ; Patent No. US20020081659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA105  
 ; CURRENT APPLICATION NUMBER: US/09/925,297  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 928  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 808

[illegible]



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RESULT 8
US-10-006-818A-180
/ Sequence 180, Application US/10006818A
/ Publication No. US20030054406A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan I.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Giang
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Gradowksi, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.

```

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; APPLICANT: PAONI, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS: Acids Encoding the Same
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 180
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-015-393A-180

Query Match      8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred. NO. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;

QY 368 SDSISITSHYKPPDCSVLSKGGDYLYKYHNASILL-DGT--LLDSTWNLGKTYNIVLGSQ 424
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 32 TREVKTEVLVLRHPENCSTKSKGDLINAHVDGYLAKDGSFKFYCSRTONEGPKPWFVIGVG 91
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 425 VVLGMDMLRECMVGKERTVIPPPLHGYGAG-VDEVGSGAVLVPDIEXLBELVAGLPEG 483
Db 92 VIKGLDIAMTDCPCGKRVIPSPFAYGKEGKIPDATLIFEI---ELYA----- 143
QY 484 YMFVNGEVSPLFEIDKNGEVLLEFFSEVHIAQVASGKGLAPGPDALIVKNMPT 543
Db 144 ---VTGPRSIETFKQIDMNDORQJSAEINLYLOREFEKDKPRDKSQ-DAVLEDFPK 199
QY 544 NDRNGDGKVTABEFLKXDOEARHD 568
Db 200 KNDHGDGDFISPKYINVY----QHD 220

RESULT 10
US-09-946-374-180
; Sequence 180, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
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;; PRIOR FILING DATE: 1998-09-24  
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;; PRIOR FILING DATE: 1998-10-08  
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;; PRIOR FILING DATE: 1998-10-20  
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;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
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;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 8.8%; Score 268; DB 9; Length 222;  
Best Local Similarity 31.2%; Pred. No. 9.2e-16;

Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;  
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DB 32 TEEVKIEVLHREPENCSTSKKGLLNNAHYDGYLAKDGSKFYCSRTQNEGHPKWFVLGVGQ 91  
QY 425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDEGVPVGSVAVLVFDIEXLELVAGLPEG 483  
DB 92 VIKGLDIAMTDMCPGKRRKVIPPSFAYGKGYAEGKIPPDATLIFEI---ELVA----- 143  
QY 484 YMFVWNGEVSFNLFEEDKNGEVLLEEFSEYTHAQVASKGLAPGFDALIVKNMFT 543  
DB 144 ---VTKGRPSITETFKQIDMDNDRLSKABINLYLQREFEKDEKPRDKSYQ-DAVLEDFK 199  
QY 544 NQDRNGDGKVTAREFKLXQEAHD 568  
DB 200 KNDHGDGDFISPKYNNVY----QHD 220

## RESULT 11

US-10-012-121A-180  
; Sequence 180, Application US/10012121A  
; Publication No. US20030073810A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC20  
; CURRENT APPLICATION NUMBER: US/10/012,121A  
; CURRENT FILING DATE: 2001-12-07  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 180  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-012-121A-180

Query Match 8.8%; Score 268; DB 9; Length 222;  
Best Local Similarity 31.2%; Pred. No. 9.2e-16;

Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;  
QY 368 SDSISITSHYKPPDCSVLSKKGYLVKHYNASLL-DGT--LLDSTWNLGKTYNIVLGSQ 424  
DB 32 TEEVKIEVLHREPENCSTSKKGLLNNAHYDGYLAKDGSKFYCSRTQNEGHPKWFVLGVGQ 91  
QY 425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDEGVPVGSVAVLVFDIEXLELVAGLPEG 483  
DB 92 VIKGLDIAMTDMCPGKRRKVIPPSFAYGKGYAEGKIPPDATLIFEI---ELVA----- 143  
QY 484 YMFVWNGEVSFNLFEEDKNGEVLLEEFSEYTHAQVASKGLAPGFDALIVKNMFT 543  
DB 144 ---VTKGRPSITETFKQIDMDNDRLSKABINLYLQREFEKDEKPRDKSYQ-DAVLEDFK 199  
QY 544 NQDRNGDGKVTAREFKLXQEAHD 568  
DB 200 KNDHGDGDFISPKYNNVY----QHD 220

## RESULT 12

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US-10-015-869A-180
; Sequence 180, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
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; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-869A-180

Query Match      8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;

QY 368 SDSISITSHYKPPDCVLSKKGDLKHYNASLL-DGT--LLDSTWNLGKTYNIVLGSQ 424
Db 32 TEVKLEVLHRPNCSTSKGDLNNAHYDGLAKDGSKYCSRTQNEGPKWFLVGQ 91

QY 425 VVLGMDMGLREMCVGKRTVIIPHLGYBAG-VDGVPVGSVAVLFDIEKLEIVAGLPEG 483
Db 92 VIKGLDIAMTDMPGKRVVIPPSPAYGKGVAEGRIPDNTLIFEI---ELVA----- 143

QY 484 YMIWNGEVSFNLFEETDKDNGEVLLEESSEYTHAQVASKGKLAPGDAELIVKNMET 543
Db 144 ---VTGPRSIETFKQIDMDNDRLQSKAEINLYLQREFEKDEKPRDKSYQ-DAVLIEDIFK 199

QY 544 NQDRNGDGKVTABEFKLXQBAKHD 568
Db 200 KNDHGDGDFISPKYNYVY----QHD 220

RESULT 13
US-09-978-295A-145
; Sequence 145, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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| PRIOR APPLICATION NUMBER: 60/084639  |  |
| PRIOR FILING DATE: 1998-05-07        |  |
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| PRIOR APPLICATION NUMBER: 60/084606  |  |
| PRIOR FILING DATE: 1998-05-07        |  |
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| PRIOR FILING DATE: 1998-05-07        |  |
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Best Local Similarity 33.0%; Pred. No. 9.7e-15;

352 SAVI.-VFDTHTVDFHNPDSISTTSHYKPPDCSVI.SKKGRVI.KYHVNASI.-IDGT7.I.DST 409

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JS-09-978-

Patent No. US20020169284A1

APPLICANT: Ashkenazi, Avi

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APPLICANT: Goddard, Audrey  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIORITY APPLICATION NUMBER: 09/918585  
PRIORITY FILING DATE: 2001-07-30  
PRIORITY APPLICATION NUMBER: 60/062250  
PRIORITY FILING DATE: 1997-10-17  
PRIORITY APPLICATION NUMBER: 60/064249  
PRIORITY FILING DATE: 1997-11-03  
PRIORITY APPLICATION NUMBER: 60/065311  
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 8.4%; Score 256; DB 9; Length 211;

Best Local Similarity 33.0%; Pred. No. 9.7e-15;

Matches 73; Conservative 38; Mismatches 88; Indels 22; Gaps 7;

QY 352 SAVL-VFDTHVDFHNPDSISITSHYKPPDCSVLSKGDYLYKHYNASL-LDGTLLDST 409

DB 7 NAVLTLFVTLICALIPEPEVKIEVLQKPFICHRKTGSDMLVHYEGYLEKDGSLFHS 66

QY 410 --WNLGKTYNVLGSGQVVLGMDMLGRLCVMGKRTVIIPHLGYGEAGVDGVPGSAYL 467

DB 67 HKHNNQPTWFTLTGILEALKGMDQGLKGMVCGEKRLIIPPALGYGKEG-KGKIPPESTL 125

QY 468 VFDIEKLEVLVAGLPEGYMTWNGEVSFNLPERIDKDGNGEVLLESEYIHAQVAGSGK 527

DB 126 IFNIDLE-----IRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEK-HGA 173

QY 528 LAPGFDAELIVKMNFTNQDRNGDKVTABEFKLXDOEAKHD 568

DB 174 VVNESHHDALVEDIFDKEDKDGFTISAREFTY-----KHD 209

RESULT 15

US-09-978-192A-145

Sequence 145, Application US/09978192A

Patent No. US20020177553A1

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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C9  
;; CURRENT APPLICATION NUMBER: US/09/978,192A  
;; CURRENT FILING DATE: 2001-10-15  
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Job time : 20.1541 secs



GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 18.1541 Seconds  
(without alignments)  
3039.596 Million cell updates/sec

Title: US-09-225-502-6  
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Scoring table: BLOSUM62  
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Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description          |
|------------|--------|-------------|--------|----------|----------------------|
| 1          | 1750.5 | 57.3        | 581    | 2 149669 | FKBP65 binding prote |
| 2          | 736    | 24.1        | 262    | 2 T42709 | hypothetical prote   |
| 3          | 382    | 12.5        | 559    | 1 S55383 | peptidylprolyl iso   |
| 4          | 344.5  | 11.3        | 261    | 2 T31741 | hypothetical prote   |
| 5          | 343    | 11.2        | 264    | 2 T29780 | hypothetical prote   |
| 6          | 311    | 10.2        | 551    | 1 S72485 | peptidylprolyl iso   |
| 7          | 307    | 10.1        | 568    | 2 T06489 | probable peptidylp   |
| 8          | 294.5  | 9.6         | 259    | 2 T27586 | hypothetical prote   |
| 9          | 286.5  | 9.4         | 139    | 2 T21882 | hypothetical prote   |
| 10         | 266.5  | 8.7         | 241    | 2 E89251 | protein ZC455.10 (   |
| 11         | 263.5  | 8.6         | 311    | 1 S46228 | peptidylprolyl iso   |
| 12         | 263    | 8.6         | 151    | 2 T12090 | probable peptidylp   |
| 13         | 262.5  | 8.6         | 304    | 2 T26538 | hypothetical prote   |
| 14         | 259.5  | 8.5         | 163    | 2 S71238 | probable peptidylp   |
| 15         | 254.5  | 8.3         | 134    | 1 J70748 | FK506-binding prot   |
| 16         | 253    | 8.3         | 146    | 1 S71237 | probable peptidylp   |
| 17         | 246    | 8.1         | 140    | 2 I49668 | binding protein -    |
| 18         | 244.5  | 8.0         | 135    | 2 S25337 | peptidylprolyl iso   |
| 19         | 242.5  | 7.9         | 142    | 2 JCI365 | FK506/rapamycin-bi   |
| 20         | 230.5  | 7.5         | 120    | 2 S11090 | FK506-binding prot   |
| 21         | 228    | 7.5         | 458    | 1 A42386 | hsp 90-binding pro   |
| 22         | 228    | 7.5         | 459    | 2 A46372 | immunophilin FKBP5   |
| 23         | 223    | 7.3         | 458    | 2 JN0873 | immunophilin p59 -   |
| 24         | 217    | 7.1         | 457    | 2 JC5422 | FK506-binding prot   |
| 25         | 214.5  | 7.0         | 113    | 2 A83180 | probable peptidyl-   |
| 26         | 212.5  | 7.0         | 165    | 2 A81878 | FKBP-type peptidyl   |
| 27         | 211.5  | 6.9         | 201    | 1 S75144 | FKBP-type peptidyl   |
| 28         | 208    | 6.8         | 152    | 2 B75347 | peptidyl-prolyl ci   |
| 29         | 207    | 6.8         | 114    | 2 A33146 | peptidylprolyl iso   |

ALIGNMENTS

RESULT 1

I49669

FKBP65 binding protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I49669

R:Simsek, S.L.; Kozak, C.A.; Winterstein, D.; Hegamyer, G.; Colburn, N.H.

Genomics 18, 407-409, 1993

A:Title: Sequence and localization of a novel FK506-binding protein to mouse chromosomes

A:Reference number: A48920; MUID:94117013; PMID:7507077

A:Accession: I49669

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581 <RES>

A:Cross-references: GB:L07063; NID:g894161; PIDN:AAC37678.1; PID:g894162

C:Superfamily: BKBP-type peptidylprolyl isomerase homology

F:61-108/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F:173-220/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>

F:285-332/Domain: BKBP-type peptidylprolyl isomerase homology <PPI3>

F:398-445/Domain: BKBP-type peptidylprolyl isomerase homology <PPI4>

Query Match 57.3%; Score 1750.5; DB 2; Length 581;

Best Local Similarity 58.9%; Pred. No. 3.8e-118;

Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY 12 PLLLLLLMW---TGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYHYVGTTPDG 68

Db 18 PLLLLQLTLERGLGRASP-AGAPLE-DWIERVHI PRACPQVQMGDFVRYHYNGTPEDG 75

QY 69 QKFDSSYDRSTFNVFVGKGLITGMDQALVGMVNERFVKIPKLAYGNRVSGVTPP 128

Db 76 KKFDDSSYDRSTLVAIVVGVRLLITGMDRLGMVNERRLIIPPHLGYSGIVAGLLPP 135

QY 129 NSVLHPDVLMDIWNSEDVQIHTYFKPPSCPRTIQVSDFVRHYNGTFLDGLTFLDSSHN 188

Db 136 DATLYFDVLLDWNKADTVQSTILLRPPYCPRMVQNSDFVRHYNGTLLDGTGFDNSYS 195

QY 189 RMKTYTYVIGIWLIPGMKGLLGMVGEKRIITIPFLAYGEDGDKDIPQASLVDPV 248

Db 196 RGGTYDTYIGSGWLIKGMDQLLGMCPGEKRIIIPFLAYGEKGYGTVIPQASLVFV 255

QY 249 ALLDLHPKDISISIEKNKVPENCERISQSGDELTYHYNGTLLDGLTFLDSSYSRRTPTDY 308

Db 256 LLLDLVHPKDTVQLETLELPQGCVRRAVAGDFMRHYNGSLMDGTFLDSSYSRHHYNTY 315

QY 309 IGQGYVTPGMDEGLLVCIGEKXIIVVPHLGVGEEGRGN-IPGSALVLFDFIHFDFNP 367

Db 316 VGGGYIIPGMDDQLGQACIGERRITVPPHLAGENGTDGKIPGSAVLIFDVHIDFNP 375

QY 368 SDSISITSHYKPPD-CSVLSKKGDKYLYKNYASLLDGLTLLDSTWNLGKTYNIVLGSQV 426

Db 376 SDPVEIKTLSPENCNCTSKIGDFIRHYNCSLLDGLTRLPSSHDEYAPQBITLGANKVI 435

hypothetical prote  
hypothetical prote  
peptidyl-prolyl ci  
FK506-binding prot  
peptidyl-prolyl ci  
peptidyl-prolyl ci  
hypothetical prote  
peptidylprolyl iso  
FK 506-binding pro  
peptide-inhibitable  
peptidylprolyl iso  
hypothetical prote  
peptidylprolyl iso  
hypothetical prote  
FKBP-type peptidyl  
peptidylprolyl iso

QY 427 LGMGLMGLREMCVGEKRTVILPHGLGYGAGVDGVPGSVAVLFDIEXLELVAGLPEGYMF 486  
 Db 436 EGLDRGLQCMVGERRQLIVPPLAHGNGARG-VPGSAVLFFVELVSREDGLPTGYLF 494  
 QY 487 IWNGEVSNNLFEEDKONGEVLLEEFSEYTHAQVASKGKGLAPGDAELIVKNNFTNQD 546  
 Db 495 VVYQDPSTSLFEDMDLNKDGVPPEEFSSFIKAQVNEGRLMPQDPDKTISDMFQND 554  
 QY 547 RNGDGKVTAEFKL---XDQEAHND 568  
 Db 555 RNQDGKTAEEELKLKSDDEQVRVHE 579

## RESULT 2

T42709

hypothetical protein DKFZp586I0821.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Sep-2000

C;Accession: T42709

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A;Reference number: Z22231

A;Accession: T42709

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-262 &lt;AAA&gt;

A;Cross-references: EMBL:AL13116

A;Experimental source: adult uterus; clone DKFZp586I0821

C;Genetics:

A;Note: DKFZp586I0821.1

C;Superfamily: BKBP-type peptidylprolyl isomerase homology

F;79-126/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI&gt;

Query Match 24.1%; Score 736; DB 2; Length 262;  
 Best Local Similarity 52.5%; Pred. No. 1.3e-45;  
 Matches 137; Conservative 53; Mismatches 65; Indels 6; Gaps 4;

QY 313 YVTPGMDGLGVCIGEKRIIVPPHGLGYGEGRGN-IPGSVAVLFDIHDVDFNPDSI 371  
 Db 1 YIIPGMDGLGVCIGEMGERRITIPPLAHGNGARG-VPGSAVLFFVELVSREDGLPTGYLFVWHK 60  
 QY 372 SITSHYKPPD-CSVLKKGDKYKHYNASLLDGTLLSTWNLGKTYNIVLGGQVILGMD 430  
 Db 61 EIKTLRSPSETNETTKLGDVFRYHYNCSLLDGTQLFTSHDYGAPQEAATLGANKVIEGLD 120  
 QY 431 MGLREMCVGEKRTVILPHGLGYGAGVDGVPGSVAVLFDIEXLELVAGLPEGYMFVWG 490  
 Db 121 TGLQCMVGERRQLIVPPLAHGNGARG-VPGSAVLFFVELVSREDGLPTGYLFVWHK 179  
 QY 491 EVSPNLFEEIDKONGEVLLEEFSEYTHAQVASKGKGLAPGDAELIVKNNFTNQDNGD 550  
 Db 180 DPPANLFEDMDLNKDGVPPEEFSTFIKAQVSEKGLMPQDPEKTIQDMFQNDQND 239  
 QY 551 GKVTAEFKL---XDQEAHND 568  
 Db 240 GKITVDELKLKSDDEQVRVHE 260

## RESULT 3

S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

N;Alternate names: FK506-binding protein; peptidylprolyl cis-trans isomerase; PPIase

C;Species: Triticum aestivum (common wheat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C;Accession: S55383

R;Oshra, B.; Breiman, A.

submitted to the EMBL Data Library, May 1995

A;Description: Wheat FKBP70 - A novel heat shock and calmodulin binding PPIase.

A;Reference number: S55383

A;Accession: S55383

A;Molecule type: mRNA

A;Residues: 1-559 &lt;OSH&gt;

A;Cross-references: EMBL:X86903; NID:g854625; PIDN:CAA60505.1; PID:g854626  
 C;Genetics:

A;Gene: FKBP70

C;Superfamily: peptidylprolyl isomerase ROP1; BKBP-type peptidylprolyl isomerase hom

C;Keywords: calmodulin binding; cis-trans isomerase; cyclosporin A binding

F;60-107/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI1&gt;

F;176-219/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI2&gt;

F;293-341/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI&gt;

F;415-448/Domain: tetratricopeptide repeat homology &lt;TT1&gt;

F;450-483/Domain: tetratricopeptide repeat homology &lt;TT2&gt;

F;484-517/Domain: tetratricopeptide repeat homology &lt;TT3&gt;

Query Match 12.5%; Score 382; DB 1; Length 559;

Best Local Similarity 30.1%; Pred. No. 1e-19;

Matches 113; Conservative 54; Mismatches 166; Indels 42; Gaps 11;

QY 50 TVRSGDFVRYHYVGFPGQKEDSSVDRDSTFNVFVGKGLITGMDOALVGMCVNERFV 109  
 Db 56 TPEVGEVEVHTGTLLDGKDFDSRRDRTFKPLGQGGVTKGWDGIGTKMKKGNALF 115  
 QY 110 KIPPKLAYGNERSVGVIIPNSVLHFDVLLMDIWNSEDQVQIHTYFKP-----PSC 159  
 Db 116 TIPPELAYGESGSPPTIPANATLQFDVELLSWTSVRDIAKGGGIFKKILKEGDKWENPKD 175  
 QY 160 PRTIQVSDFVRYHYNGTFLDGTLPDSSHNRMTYDTYVIGWLIIPGMDKGLLGMCVGEKR 219  
 Db 176 P-----DEVFVKYEARELDGTWVSKSEG----VEFTVKDGHLCPALAKAVTKMKGEKV 225  
 QY 220 IITIPPFLAYGE-----DQDGDKI PQQASLVDFDVALLD---LHNPKDSISIEKVVVP--E 269  
 Db 226 LLAVKPOYGFGEGRPAAGEGAVPNASLVLDLDELVSWKVTTEIGDDKKILKKVLEKE 285  
 QY 270 NCERISQSGDFLTTHYNGTLLDGTLP-DSSVSRNRTFTYIQGVYIPGMDGLLGVCI 328  
 Db 286 GYERFNE-GAVTVTKITGLQDGTIVLKKGHDEQEPFEKTDDEAVIEGLDRAVLNWK 344  
 QY 329 EKRXIVVPHLGYGE-EGRGN--IPGSVAVLFDIHDVDFNPDSISITSH-----YK 378  
 Db 345 EVALVTIPPEYAYGSTESKQDAIVPNSTVIYVELSVFVKDESWDLNNSKEIAAGTK 404  
 QY 379 PPDCSVLSKKGDIYK 393  
 Db 405 KEEGNALFKSGKYAR 419

## RESULT 4

T31741

hypothetical protein C05C8.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 02-Sep-2000

C;Accession: T31741

R;Sammons, L.; Wohldmann, P.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of C. elegans cosmid C05C8.

A;Reference number: Z21078

A;Accession: T31741

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-261 &lt;SAM&gt;

A;Cross-references: EMBL:AF016430; PIDN:AAB65370.1; GSPDB:GN00023; CBSP:C05C8.3

A;Experimental source: strain Bristol N2; clone C05C8

C;Genetics:

A;Gene: C05C8.3

A;Map position: 5

A;Introns: 119/3

C;Superfamily: BKBP-type peptidylprolyl isomerase homology

F;48-94/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI1&gt;

F;166-213/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI2&gt;

Query Match

11.3%; Score 344.5; DB 2; Length 261;

Best Local Similarity

32.2%; Pred. No. 1.8e-17;

Matches 73; Conservative

51; Mismatches 92; Indels

11; Gaps

4;





Db 34 ITTSSIDSECEIKSAGDVVDQYKLTDEKGVIGSNFGK-KPYTFTLGRNQVPGMD 92  
QY 320 EGLGVCIGEKRXIIVPPHLCVGEGRNIPGSAVLVDIHDVDFH--NP-----SDSI 371  
Db 93 RAMGMCIGERIKRVIPPKVGFADSTCQ-----PLYTVQLVNLFRANPGRWTEGII 147  
QY 372 SITSHYK-PPDCSVLSKGDYKHYNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMD 430  
Db 148 QIDQIHKEADCKKARAGDKIYQOYVLRLENTL-----EVIDGMD 189  
QY 431 MGLREMCGEKRTVILPHLHGGEAGVDGVEPGSAVLVDFIEKLELV 477  
Db 190 IAMDGMCEGERRRVIPSEYGYGSGSPPEIPGGARLFFEIVLEKLV 236

## RESULT 11

S46228

peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus

N;Alternate names: fkbB protein

C;Species: Streptomyces chrysomallus

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: S46228

R;Fahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FKs

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46228

A;Molecule type: DNA

A;Residues: 1-311 &lt;PAH&gt;

A;Cross-references: GB:234523; NID:G535270; PIDN:CAA84280.1; PID:G633644

A;Experimental source: ATCC 11523

C;Genetics:

A;Gene: fkbB

C;Superfamily: peptidylprolyl isomerase FKBP33; BKBp-type peptidylprolyl isomerase homol

F;1-18/Domain: blocked amino end; cis-trans-isomerase; lipoprotein

F;19-311/Product: signal sequence #status predicted &lt;SIG&gt;

F;77-125/Domain: BKBp-type peptidylprolyl isomerase FKBP-33 #status predicted &lt;MAT&gt;

F;224-271/Domain: BKBp-type peptidylprolyl isomerase homology &lt;PPI1&gt;

F;19/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

F;19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted

Query Match 8.6%; Score 263.5; DB 1; Length 311;  
Best Local Similarity 27.6%; Pred. No. 1.6e-11;  
Matches 84; Conservative 49; Mismatches 100; Indels 71; Gaps 11;

QY 212 GMCVGEKRIITIPPLAYGEGDGDIPGQASLVDFVALLDLHNPDKSISIKVVPENC 271

Db 41 GAKFGEK-----PTLSKGE-GD-----PPKE---LKTDTVISEGD 70

QY 272 ERISQSGDLTYHNGTLLDGLT-PDSSYSRNRFTDTYIGQYVIPGMDGGLGVCIGEK 330

Db 71 GAKLNGDAIQVYLGQAWDSTKPFNSFDRKQPPDLTLGAGMVIQGWMDKGLVGKVGSR 130

QY 331 RXIIVPPHLCVGEGRNIPGSAVLVDFIHI-----PPKE----- 362

Db 131 VELVIPPELGVGEGQGDIKENATLVFVVDILKATQIPASAKGTEVAQDNVDLPKVGVT 190

QY 363 DFHNPSDSI-----SITSHYKPPDCSVLSKGDYKHYNASLLDGLT-LDSTWNLGK 414

Db 191 DGKAPTIVTPKSDPPKLVSNVLESDEGVVKSDESVVYVGMWIKGAKBFDNYITGK 250

QY 415 TYNIVLGSQVVL-GMDNGLREMCGEKRTVILPHLHGGEAGVDGVEPGSAVLVDFIEK 473

Db 251 TQTPLP--SQVTLKGLKNGLIDKKVGSRVLLVIPPDAQFGDQOQQA-IPKNSTLVFAVDI 307

QY 474 LELV 477

Db 308 LAKV 311

## RESULT 12

T12090  
probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15 precursor - fava bean  
N;Alternate names: FK506-binding protein; immunophilin; rapamycin-binding protein  
C;Species: Vicia faba (fava bean)  
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 21-Jul-2000  
C;Accession: T12090  
R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.  
Proc. Natl. Acad. Sci. U.S.A. 93, 6964-6969, 1996  
A;Title: Molecular characterization of a FKBP-type immunophilin from higher plants.  
A;Reference number: Z17411; MUID:96293457; PMID:8692927  
A;Accession: T12090  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-151 <LUA>  
A;Cross-references: EMBL:U52045; NID:G1272409; PIDN:AAC49392.1; PID:G1272410  
C;Genetics:

A;Gene: FKBP15

A;Note: Inhibited by immunosuppressant drugs FK506 and rapamycin

C;Superfamily: BKBp-type peptidylprolyl isomerase; BKBp-type peptidylprolyl isomerase

C;Keywords: cis-trans-isomerase; cyclosporin A binding; immunoregulation

F;1-22/Domain: signal sequence #status predicted &lt;SIG&gt;

F;23-151/Product: peptidylprolyl isomerase FKBP15 #status predicted &lt;MAT&gt;

F;49-96/Domain: BKBp-type peptidylprolyl isomerase homology &lt;PPI&gt;

Query Match 8.6%; Score 263; DB 2; Length 151;  
Best Local Similarity 42.1%; Pred. No. 6.4e-12;  
Matches 56; Conservative 22; Mismatches 47; Indels 8; Gaps 3;

QY 244 LVFDV-----ALLDLHNPDK--SISIENKVVPENCERISQSGDLTYHNGTLLDGLTLD 296

Db 8 LIPTFIASALVAAKSAADVTELQIGVKYKPASCEVQAHKGDVKVHYRGKLTGDTGTFD 67

QY 297 SSYSRNRFTDTYIGQYVIPGMDGGLGVCIGEKRXIIVPPHLCVGEGR-GNIPGSAVL 355

Db 68 SSFERNSPDIFELGQGVVTKGMDQGLGMLGCKRKLKIPAKLGYGSGSPPTIPGGATL 127

QY 356 VFDDHVIDFHNPS 368

Db 128 IFDTELGVNDKS 140

## RESULT 13

T26538

hypothetical protein Y18D10A.19b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 28-Jul-2000

C;Accession: T26538

R;Harris, B.

A;Reference number: Z20226

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-304 &lt;WIL&gt;

A;Cross-references: EMBL:AL034393; PIDN:CAA22329.1; CESP:Y18D10A.19b

A;Experimental source: clone Y18D10A

C;Genetics:

A;Gene: CESP:Y18D10A.19b

A;Introns: 82/1; 148/3; 195/1; 262/3

C;Superfamily: BKBp-type peptidylprolyl isomerase homology

F;102-149/Domain: BKBp-type peptidylprolyl isomerase homology &lt;PPI1&gt;

F;216-263/Domain: BKBp-type peptidylprolyl isomerase homology &lt;PPI&gt;

Query Match 8.6%; Score 262.5; DB 2; Length 304;  
Best Local Similarity 27.0%; Pred. No. 1.8e-11;  
Matches 96; Conservative 43; Mismatches 148; Indels 69; Gaps 9;

QY 129 NSVLHFDVLLMDIWNSEDQVQIHTYFKPSCPRTIQVDFVRHYNGTFLDGLTFDSSH 188

Db 5 NGVASTDDSVLPFSWNPVGQ-----FIVSTYNEYEYKRIFFPRELEFGCLLC 51

QY 189 RMKTYDTYVIGWLIPQMDKGLLGMCVGEKRIITIPPLAYGEDGDKDIPGQASLVFDV 248

Db 52 RMRFTNH-----EGMKHLRDHVHVK-----SSCEHEKPKGT----- 85  
Qy 249 ALLDLNPKDSISIEKNKVPENCERISQSGDPLTHYNGTLLDGTLPDSSYSRNRTFTDY 308  
Db 86 ----IHHQVDKAG--NGVMPEN-----GOLVQCYIEIKLADCYTSWSNYESQNPPIPK 132  
Qy 309 IGGYVPIPMDEGLLVCIGEKRXIVPPHLYGGEGR--RGNIPGSAVLVFDIHVDFHNP 367  
Db 133 IGFGEVPIGLDIGIPKMKVGEIATFVSGKYGGRAGFGLIPRNASLTCKVLF----- 187  
Qy 368 SDSISITSHVK-----PPDCSVLSKKGDYLYKYNHNASLDDGTLLDSTWNLGKTYNI 418  
Db 188 --NCSWDSYAKIGVDRQILVQGNVTXKNGQFVTCHYVLVLVDGTAKIDSSRDRETPKF 245  
Qy 419 VLGSGOVVLGMDGLREMCVGEKRTVLIIPHLGYGEAGVGEVPGSAVLVFDIEXL 474  
Db 246 KTGKGEVIGWGDQGVQMSVGEKSKLTISADLGYGPRGVPQIPANATLVFEVELL 301

## RESULT 14

S71238

Probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliana

N;Alternate names: FK-binding protein 15-2; immunophilin

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 16-Jul-1999

C;Accession: S71238

R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.

submitted to the EMBL Data Library, March 1996

A;Description: Molecular characterization of a FKBP-type immunophilin from higher plants

A;Reference number: S71238

A;Accession: S71238

A;Molecule type: mRNA

A;Residues: 1-163 &lt;LUA&gt;

A;Cross-references: EMBL:U52047; NID:g1272407; PIDN:AAC49391.1; PID:g1272408

C;Genetics:

A;Gene: FKBP15-2

C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase ho

C;Keywords: cis-trans-isomerase

F;52-99/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI&gt;

## Query Match

8.5%; Score 259.5; DB 2; Length 163;

Best Local Similarity 48.1%; Pred. No. 1.3e-11;

Matches 50; Conservative 15; Mismatches 38; Indels 1; Gaps 1;

Qy 260 ISIEKNKVPENCERISQSGDPLTHYNGTLLDGTLPDSSYSRNRTFTDYIGQGVIPGMD 319

Db 34 LQGVKFKPTCVQAHKGDTIKVHVGKLTGDFVDFSSFERGDPFPEFKLGSGQVIKGMW 93

Qy 320 EGLLVCIGEKRXIVPPHLYGGEGR--GNIPGSAVLVFDIHVI 362

Db 94 QGLGACVGEKKLTKIPAKLGYGEQSGSPPTIPGATLIFDTIELI 137

## RESULT 15

JT0748

FK506-binding protein - Botryllus schlosseri

C;Species: Botryllus schlosseri

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: JT0748; S40074

R;Pancer, Z.; Gershon, H.; Rinkevich, B.

Biochem. Biophys. Res. Commun. 197, 973-977, 1993

A;Title: cDNA cloning of a putative protochordate FK506-binding protein.

A;Reference number: JT0748; MUID:94092189; PMID:7505578

A;Accession: JT0748

A;Molecule type: mRNA

A;Residues: 1-134 &lt;PAN&gt;

A;Cross-references: EMBL:X76006; NID:g435470; PIDN:CAA53594.1; PID:g435471

C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase ho

F;41-88/Domain: BKBP-type peptidylprolyl isomerase homology &lt;PPI&gt;

## Query\*Match

8.3%; Score 254.5; DB 1; Length 134;

Best Local Similarity 52.7%; Pred. No. 2.2e-11;

Matches 49; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

Qy 271 CERISQSGDPLTHYNGTLLDGTLPDSSYSRNRTFTDYIGQGVIPGMDLGLVCIGBK 330  
Db 34 CERKSGGVDLMDHHTGTLEDGSKFDSRRDFTFTTLGGQYVIKGMWKGLLGMCBGER 93  
Qy 331 RXIVVPPHLYGGEGR--GNIPGSAVLVFDIHVI 362  
Db 94 RKLKIPSDMGYGRGSPFPKIPGGATLIFDVELL 126

Search completed: April 26, 2003, 06:50:55

Job time : 20.1541 secs



GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:55 ; Search time 10.2323 Seconds  
(without alignments)  
2326.688 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAFRGWRPPPPPLLLLLLV.....AEFKLXQAKHDVTLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 1750.5 | 57.3        | 581    | 1     | FKB3_MOUSE  |
| 2          | 382    | 12.5        | 559    | 1     | FKB7_WHEAT  |
| 3          | 246    | 8.1         | 140    | 1     | FKB2_MOUSE  |
| 4          | 244.5  | 8.0         | 135    | 1     | FKB2_YEAST  |
| 5          | 234.5  | 7.7         | 217    | 1     | FK21_NEUCR  |
| 6          | 231.5  | 7.6         | 141    | 1     | FKB2_HUMAN  |
| 7          | 230.5  | 7.5         | 120    | 1     | FKBP_NEUCR  |
| 8          | 228    | 7.5         | 457    | 1     | FKB4_RABIT  |
| 9          | 228    | 7.5         | 458    | 1     | FKB4_HUMAN  |
| 10         | 223    | 7.3         | 457    | 1     | FKB5_MOUSE  |
| 11         | 217    | 7.1         | 457    | 1     | FKB5_HUMAN  |
| 12         | 210.5  | 6.9         | 456    | 1     | FKB5_MOUSE  |
| 13         | 207    | 6.8         | 114    | 1     | FKBP_YEAST  |
| 14         | 196    | 6.4         | 112    | 1     | FKBP_SCHPO  |
| 15         | 195.5  | 6.4         | 108    | 1     | FKB1_DROME  |
| 16         | 191    | 6.3         | 208    | 1     | FKB3_ARATH  |
| 17         | 184    | 6.0         | 268    | 1     | FKBA_AERYH  |
| 18         | 178    | 5.8         | 107    | 1     | FKB1_XENLA  |
| 19         | 176    | 5.8         | 107    | 1     | FKB1_BOVIN  |
| 20         | 174.5  | 5.7         | 109    | 1     | FKBP_NEIMA  |
| 21         | 172.5  | 5.6         | 107    | 1     | FKB1_RAT    |
| 22         | 172.5  | 5.6         | 109    | 1     | FKBP_NEIMB  |
| 23         | 171.5  | 5.6         | 107    | 1     | FKB1_HUMAN  |
| 24         | 171.5  | 5.6         | 270    | 1     | FKBA_ECOLI  |
| 25         | 171    | 5.6         | 205    | 1     | FKBB_ECOLI  |
| 26         | 171    | 5.6         | 241    | 1     | FKBY_HAETN  |
| 27         | 170    | 5.6         | 107    | 1     | FKBB_RAT    |
| 28         | 168    | 5.5         | 107    | 1     | FKBB_HUMAN  |
| 29         | 167    | 5.5         | 241    | 1     | FKBA_BUCAL  |
| 30         | 164    | 5.4         | 107    | 1     | FKB1_MOUSE  |
| 31         | 155    | 5.1         | 411    | 1     | FKB3_YEAST  |
| 32         | 154.5  | 5.1         | 224    | 1     | FKB3_MOUSE  |
| 33         | 153    | 5.0         | 124    | 1     | FKBP_STRCH  |

## ALIGNMENTS

| RESULT 1   |  |            |           |      |            |        |             |  |  |
|------------|--|------------|-----------|------|------------|--------|-------------|--|--|
| FKBX_MOUSE | ID   | FKBX_MOUSE | STANDARD; | PRT; | 581 AA.    |        |             |  |  |
| AC         | Q61576;  | 5.0        | 224       | 1    | FKB3_BOVIN | P26884 | bos taurus  |  |  |
| DT         | 30-MAY-2000 (Rel. 39, Created)   | 5.0        | 243       | 1    | MIP_CHLTR  | P26223 | chlamydia t |  |  |
| DT         | 30-MAY-2000 (Rel. 39, Last sequence update)  | 4.9        | 223       | 1    | FKB3_RABIT | Q06638 | oryctolagus |  |  |
| DT         | 16-OCT-2001 (Rel. 40, Last annotation update)  | 4.9        | 224       | 1    | FKB3_HUMAN | Q06688 | homo sapien |  |  |
| DE         | 65 kDa FK506-binding protein precursor (SC 5.2.1.8) (FKBP65) (FKBPRP)  | 4.7        | 392       | 1    | FKB4_YEAST | Q06205 | saccharomyc |  |  |
| DE         | (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)  | 4.7        | 124       | 1    | FKBP_CANAL | P28870 | candida alb |  |  |
| DE         | (Immunophilin FKBP65)  | 4.6        | 357       | 1    | FKB4_DROME | P54397 | drosophila  |  |  |
| GN         | FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP.   | 4.6        | 361       | 1    | FKB4_SCHPO | Q74191 | schizosacch |  |  |
| OS         | Mus musculus (Mouse).  | 4.5        | 243       | 1    | MIP_CHLMU  | Q9PJ11 | chlamydia m |  |  |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  | 4.5        | 362       | 1    | YAV6_SCHPO | Q10175 | schizosacch |  |  |
| OC         | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   | 4.4        | 223       | 1    | FKB2_ARATH | O28870 | arabidopsis |  |  |
| OX         | NCBI_TaxID=10090;  | 4.4        | 258       | 1    | MIP_CHLPN  | Q927p3 | chlamydia p |  |  |
| RN         | [1]  |            |           |      |            |        |             |  |  |
| RP         | SEQUENCE FROM N.A.   |            |           |      |            |        |             |  |  |
| RC         | STRAIN=JBG; TISSUE=Epidermis;  |            |           |      |            |        |             |  |  |
| RX         | MEDLINE=94117013; PubMed=7507077;  |            |           |      |            |        |             |  |  |
| RA         | Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;   |            |           |      |            |        |             |  |  |
| RT         | "Sequence and localization of a novel FK506-binding protein to mouse   |            |           |      |            |        |             |  |  |
| RT         | chromosome 11.";   |            |           |      |            |        |             |  |  |
| RL         | Genomics 18:407-409(1993).   |            |           |      |            |        |             |  |  |
| [2]        |  |            |           |      |            |        |             |  |  |
| RP         | SEQUENCE FROM N.A., AND CHARACTERIZATION.  |            |           |      |            |        |             |  |  |
| RN         | MEDLINE=96094328; PubMed=7493967;  |            |           |      |            |        |             |  |  |
| RX         | Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;   |            |           |      |            |        |             |  |  |
| RA         | "Molecular cloning, DNA sequence analysis, and biochemical   |            |           |      |            |        |             |  |  |
| RT         | characterization of a novel 65-kDa FK506-binding protein (FKBP65).";   |            |           |      |            |        |             |  |  |
| RL         | J. Biol. Chem. 270:29336-29341(1995).  |            |           |      |            |        |             |  |  |
| CC         | - FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING  |            |           |      |            |        |             |  |  |
| CC         | PROTEIN SYNTHESIS.   |            |           |      |            |        |             |  |  |
| CC         | - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  |            |           |      |            |        |             |  |  |
| CC         | PEPTIDE BONDS IN OLIGOPEPTIDES.  |            |           |      |            |        |             |  |  |
| CC         | - ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT  |            |           |      |            |        |             |  |  |
| CC         | BY CYCLOSPORINE A.   |            |           |      |            |        |             |  |  |
| CC         | - SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL).   |            |           |      |            |        |             |  |  |
| CC         | - TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN  |            |           |      |            |        |             |  |  |
| CC         | AND TESTIS.  |            |           |      |            |        |             |  |  |
| CC         | - PTM: GLYCOSYLATED AND PHOSPHORYLATED.  |            |           |      |            |        |             |  |  |
| CC         | - SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4   |            |           |      |            |        |             |  |  |
| CC         | FKBP-LIKE DOMAINS.   |            |           |      |            |        |             |  |  |
| CC         | - SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  |            |           |      |            |        |             |  |  |
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| CC         | the European Bioinformatics Institute. There are no restrictions on its  |            |           |      |            |        |             |  |  |
| CC         | use by non-profit institutions as long as its content is in no way   |            |           |      |            |        |             |  |  |
| CC         | modified and this statement is not removed. Usage by and for commercial  |            |           |      |            |        |             |  |  |
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| CC         | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |            |           |      |            |        |             |  |  |
| CC         |  |            |           |      |            |        |             |  |  |
| CC         |  |            |           |      |            |        |             |  |  |
| CC         | EMBL; L07063; AAC37678.1; --   |            |           |      |            |        |             |  |  |
| CC         | HSSP; P20081; LYAT.  |            |           |      |            |        |             |  |  |
| CC         | MGD; MGI:104769; Fkbp6.  |            |           |      |            |        |             |  |  |
| CC         | InterPro; IPR002048; EF-hand.  |            |           |      |            |        |             |  |  |

```
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; Efh; 2.
DR PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00059; FKBP_PPIASE 3; 4.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00018; EF_HAND; 1.
KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 33
FT CHAIN 34 581
FT DOMAIN 54 146
FT DOMAIN 179 258
FT DOMAIN 291 370
FT DOMAIN 389 482
FT CA_BIND 509 520
FT CA_BIND 554 565
FT CARBOHYD 69 69
FT CARBOHYD 181 181
FT CARBOHYD 293 293
FT CARBOHYD 309 309
FT CARBOHYD 351 351
FT CARBOHYD 392 392
FT CARBOHYD 406 406
FT SITE 578 581
SQ SEQUENCE 581 AA; 64669 MW; 1B51B302089F555 CRC64;

Query Match 57.3%; Score 1750.5; DB 1; Length 581;
Best Local Similarity 58.9%; Pred. No. 3.8e-119;
Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY 12 PLILLILLWV---TQAAIPVAGLSDELQIERFVDECPRTVRSQDFVRYHYGTFPDG 68
Db 18 PLLLLQLTLELGRASP-AGAPLE-DVVIERVHIPRACPREVQMGDFVRYHYNGTFEDG 75
QY 69 QKFDSSYDRDSTFNVPVFGKQLITGMDQALVGMVNERRPVKIPPKLAYGNERSGVIPP 128
Db 76 KKFDSYDSTLVAIVVGVRLITGMDRLGMLCMVNERRLIVPPHLYGSGIVAGLIPP 135
QY 129 NSVLHPDLVLMINSEDOVQIHTYFKPPSCPTIQVDFVRYHYNGTFDGLDGLFDSHSHN 188
Db 136 DATLYDFVLLVWKNADTVQSTILLRPPYCPRMVQNSDFVRHYNGTLLDGLTGFDNSYS 195
QY 189 RMKTYDTYVIGWILPGMDKGLLGMVCGEKRIITIPFLAYGEDGDKDIPGOASLVFDV 248
Db 196 RGTYDTYIGSGWLIKGMDOGLLGMVCGEKRIITIPFLAYGKGYGTVIPPQASLVFVY 255
QY 249 ALLDLHNPXDSISIEKNVVPENCERISQSGDFTYHYNGTLLDGLDGLFDSYSERNRTFDY 308
Db 256 LLLDLVHNPXDTVQLETLLELPQGVRAVAGDFRYHYNGSLMDGLTFLDSSYSRNHTYNTY 315
QY 309 IQGVVPIGMDGLLGVCTIGEKRXIIVPPHLYGGEGRGN-IPGSALVFDIHDVDFHNP 367
Db 316 VGQGYIIPGMDQGLQACIGERRRITVPPHLYAGENGARG-VPGSAVLVFDVHVDHNP 375
QY 368 SDISITSHYKPD-CVLSKKGDKYLYKHYNASLLDGLTLLDSTWNLGKYNIVLGSQGVV 426
Db 376 SDPVEIKLSRPENCNETSIGDFIRHYNCSLLDGLTFLFSSHDEYAPQEITLGANKVI 435
QY 427 LGMDGLREMCVGEKRTVIIPPHLYGGEAGVGEVPGSAVLVFDIEKLELVAGLPGGYMF 486
Db 436 EGLDRGLQMGVRRQLIVPPHLYAGENGARG-VPGSAVLVFEVLVSRDGLPTGYLF 494
QY 487 IWNGEVSNLPEIKDNGEVLLEBFSEYIIHQVAASGKGKAPGPDABLIVKQMTNQD 546
Db 495 VVYQDPSTLFDMDLNKDGVEPPPEFSSFIKAQVNEGKRLMPGDPDKTISDMFQND 554
QY 547 RNGDGKVTAEKFL---XDOEAKHD 568
Db 555 RNQDGKITAELKLKLSDEDEOERVHE 579
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RESULT 2
FKB7 WHEAT STANDARD; PRT; 559 AA.
ID Q43207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
isomerase) (Cyclophilin) (PPIase).
GN FKBP70.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATIR; TISSUE=Root tip;
RA Oshra B., Breiman A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASE THAT BINDS CALMODULIN.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC -----
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CC -----
DR EMBL; X86903; CAA60505.1; -.
DR HSSP; P27124; 1ROT.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 3.
DR Pfam; PF00515; TPR; 3.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00453; FKBP_PPIASE 1; 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; 3.
DR PROSITE; PS00059; FKBP_PPIASE 3; 3.
KW Isomerase; Rotamase; Repeat; TPR repeat; Heat shock;
KW Calmodulin-binding.
FT DOMAIN 60 148 PPIASE, FKBP-TYPE 1.
FT DOMAIN 176 265 PPIASE, FKBP-TYPE 2.
FT DOMAIN 293 384 PPIASE, FKBP-TYPE 3.
FT REPEAT 401 434 TPR 1.
FT REPEAT 450 483 TPR 2.
FT REPEAT 484 517 TPR 3.
SQ SEQUENCE 559 AA; 62056 MW; 5C5DAE70D716B541 CRC64;

Query Match 12.5%; Score 382; DB 1; Length 559;
Best Local Similarity 30.1%; Pred. No. 3e-20;
Matches 113; Conservative 54; Mismatches 166; Indels 42; Gaps 11;

QY 50 TVRSQDFVRYHYGTFPDGQKFDSSYDRDSTFNVPVFGKQLITGMDQALVGMVNERFV 109
Db 56 TPEVSGDEVHYHTGTLDDGKGFSSRRDDTFFKLGQGVKIGWDQGIKTKKGENALF 115
QY 110 KIPPKLAYGNERSGVIPNSVLHFDVLLMDINSEDOVQIHTYFKP-----PSC 159
Db 116 TTPPELAYGESGPPPIPANATLQFDVLLSWTSVRIADKDGIFKILKEGDKWENPKD 175
QY 160 PRTIQVSDPVRHYNGTFLDGLTFLDSSHNRMTYDTYVIGIWLPMDKGLLGMVCGEK 219
Db 176 P-----DEVFVKYEARLEDGTVVSKSEG----VEFTVKDGHLCPALAKAVKTMKGEK 225
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Query Match 8.1%; Score 246; DB 1; Length 140;  
 Best Local Similarity 34.3%; Pred. No. 3.6e-11;  
 Matches 59; Conservative 25; Mismatches 52; Indels 36; Gaps 5;

QY 220 IITIPPPLAYGE-----DGDGKDIPGQASLVFVALD---LHNPDKSISTENKVP--B 269  
 DB 226 LIAVKFOYGFGEGRPAAGGAVPPNASLIVDLEVSWKTVEIGDDKKILKKVLKXEXE 285

QY 270 NCRISQSGDFTLYHYNGTLLDGLTF--DSSYSRNRTPDTYIGQYVWPGMDGGLGVCIG 328  
 DB 286 GYERPNE-GAVTVTKITGKLDGTFTVFLKKGHDEQEPFEFTDEAVIEGLDRAVLNKKG 344

QY 329 EKRXIVVPHLGYGE-EGRN--IPGSAVLVFDIHVIDFNPSDSISITSH-----YK 378  
 DB 345 EVALVTIPPEYAYGTESTEKQDAIVPPNPTVYVELSVFVKDKESWDLNNSIEKTEAAGTK 404

QY 379 PDCSVLSKKGDKLK 393  
 DB 405 KEEGNALFRSGKYAR 419

## RESULT 3

FKB2 MOUSE  
 ID FKB2 MOUSE STANDARD; PRT; 140 AA.  
 AC P45878;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).  
 GN FKBP2 OR FKBP13.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Liver;  
 RX MEDLINE=94085790; PubMed=7505249;  
 RA Hendrickson B.A.; Zhang W.; Craig R.J.; Jin Y.J.; Bierer R.E.; Burakoff S.J.; Dilella A.G.;  
 RT "Structural organization of the genes encoding human and murine FK506-binding protein (FKBP) 13 and comparison to FKBP1.";  
 RL Gene 134:271-275(1993).  
 CC -!- FUNCTION: PPIases accelerate the folding of proteins. May function as a component of membrane cytoskeletal scaffolds.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.  
 CC -!- SUBUNIT: Interacts with the C-terminal domain of 4.1G.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC  
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 CC  
 CC EMBL; M77831; AAA37631.1; -  
 CC HSSP; P20081; 1YAT.  
 CC MGD; MGI:95542; FKBP2.  
 CC InterPro; IPR001179; FKBP\_PPIase.  
 CC Pfam; PF00254; FKBP; 1.  
 CC PROSITE; PS00453; FKBP\_PPIASE 1; 1.  
 CC PROSITE; PS00454; FKBP\_PPIASE 2; 1.  
 CC PROSITE; PS00059; FKBP\_PPIASE 3; 1.  
 CC Isomerase; Rotamase; signal; Endoplasmic reticulum.  
 CC SIGNAL 1 22 POTENTIAL.  
 CC CHAIN 23 140 FK506-BINDING PROTEIN.  
 CC SITE 137 140 PREVENT SECRETION FROM ER (POTENTIAL).  
 CC SEQUENCE 140 AA; 15344 MW; F4E7FCC7766A0416 CRC64;

Query Match 8.1%; Score 246; DB 1; Length 140;  
 Best Local Similarity 34.3%; Pred. No. 3.6e-11;  
 Matches 59; Conservative 25; Mismatches 52; Indels 36; Gaps 5;

QY 199 IGWLPGMDKGLGCMVCGEKRIITPPPLAYGEDGDKDIPGQASLVFVALDLHNPXD 258  
 DB 3 LSWILT-----ILSICLSA-----LAAATGAEGK-----RKL 29

QY 259 SISTENKVVPCERISQSGDFTLYHYNGTLLDGLTFDSSYSRNRTPDTYIGQYVWPGM 318  
 DB 30 QIGVKRY--DHCPTKSRKGDVHLHMYTKLEDGTEFDSLPQNPQFVSLGTGVKIGW 87

QY 319 DEGLGVCIGKRXIIVVPHLGYGEGR--GNIPGSAVLVFDIHVIDFNHPSD 369  
 DB 88 DQGLGMCGEGRKLVIPSELGYGEGAPPKIPGGATLVFEVELLKIERSE 139

RESULT 4  
 FKB2 YEAST  
 ID FKB2 YEAST STANDARD; PRT; 135 AA.  
 AC P32472;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).  
 GN FPR2 OR FKB2 OR YDR519W OR D9719.24.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93070605; PubMed=1279908;  
 RA Partridge J.A.; Fleming M.A.; Harding M.W.; Berlin V.;  
 RT "Saccharomycetes cerevisiae contains a homolog of human FKBP-13, a membrane-associated FK506/zapamycin binding protein.";  
 RL Yeast 8:673-680(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-54.  
 RX MEDLINE=92366483; PubMed=1380159;  
 RA Nielsen J.B.; Poor F.; Sierkerka J.J.; Hsu M.J.; Ramadan N.;  
 RA Moxin N.; Shafiee A.; Dahl A.; Brizuela L.; Chretien G.;  
 RA Bostian K.A.; Parent S.A.;  
 RT "Yeast FKBP-13 is a membrane-associated FK506-binding protein encoded by the nonessential gene FKB2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7471-7475(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Dietrich F.S.; Mulligan J.; Allen E.; Araujo R.; Aviles E.;  
 RA Berno A.; Carpenter J.; Chen E.; Cherry J.M.; Chung E.; Duncan M.;  
 RA Hunnicke-Smith S.; Hyman R.; Komp C.; Lashkari D.; Lew H.; Lin D.;  
 RA Mosedale D.; Nakahara K.; Namath A.; Oefner P.; Oh C.; Petel F.X.;  
 RA Roberts D.; Schramm S.; Schroeder M.; Shogren T.; Shroff N.;  
 RA Winant A.; Yelton M.; Botstein D.; Davis R.W.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKBP-13 MAY PLAY A ROLE IN PROTEIN TRAFFICKING IN THE ER.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.  
 CC -!- BINDS FK506 WITH 15-FOLD LOWER AFFINITY THAN FKB1.  
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. IS NOT SECRETED AND PROBABLY LOCALIZED IN THE ENDOPLASMIC RETICULUM.  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC  
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CC -----
DR EMBL; M30767; AAA34604.1; -
DR EMBL; M30767; AAA34605.1; -
DR EMBL; U33057; AAB64960.1; -
DR PIR; S25337; S25337.
DR PIR; A46154; A46154.
DR HSSP; P20081; LYAT.
DR SGD; S000297; FKBP2.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP, 1.
DR PROSITE; PS00453; FKBP_PPIASE 1; 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00509; FKBP_PPIASE 3; 1.
KW Isomerase; Rotamase; Signal; Endoplasmic reticulum.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 135 FK506-BINDING PROTEIN.
FT SEQUENCE 135 AA; 14487 MW; 09CA3F1568D7E4B4 CRC64;

Query Match 8.0%; Score 244.5; DB 1; Length 135;
Best Local Similarity 43.3%; Pred. No. 4.4e-11;
Matches 55; Conservative 21; Mismatches 50; Indels 1; Gaps 1;

QY 16 LLLVWTGQAPVAGLSDAELQIERRVDPDECRPTVRSQDFVRVHYVGT.FPDGQKFDSS 74
Db 5 IYLFVTFSTILAGSLSDLEIGIKRIPVEDCLIKAMPDKVKVHYTGSLLSGTDFSS 64

QY 75 YDRDSTFNVFVGQGLITGMDQALVGMVNERFRVKIPPKLAYGNERSVGVIPNSVLHF 134
Db 65 YRSGSFIAPELGVRVKGWDQVAGMCGVKRKLQIPSSLAYGERGVGVIPPSADLVF 124

QY 135 DVLVMDI 141
Db 125 DVELVDV 131

RESULT 5
FK21 NEUCR
ID FK21 NEUCR STANDARD; PRT; 217 AA.
AC O60046;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FK506-binding protein precursor (FKBP-21) (Peptidyl-prolyl cis-
trans isomerase) (PPIase) (EC 5.2.1.8).
GN FKBP-21.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RA Solascheid B., Tropisch M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; J006297; CAA06962.1; -
DR HSSP; AQ0688; 1PBK.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.

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DR PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00509; FKBP_PPIASE 3; 1.
DR PROSITE; PS00014; ER TARGET; 1.
KW Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 217 FK506-BINDING PROTEIN.
FT SITE 214 217 PREVENT SECRETION FROM ER (POTENTIAL).
FT SEQUENCE 217 AA; 22915 MW; 72313067521BCDAF CRC64;

Query Match 7.7%; Score 234.5; DB 1; Length 217;
Best Local Similarity 46.4%; Pred. No. 4.2e-10;
Matches 45; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

QY 267 VPENCERISQSGDLTVHYNGTL-LDGLTFDSSYSRNRFTDTYIGQYVPGMDEGLGV 325
Db 30 VPVECDRKTRKGDKNVHYRGTLSNQGFDAVDYRGTPFSPKLGQGVKMGWDEGLVDM 89

QY 326 CIGEKXIVVPHLYGEGEGNIPGSALVFDHVI 362
Db 90 CIGEKRTLTVPSPYGYGQSGIPAGSTLIFETELI 126

RESULT 6
FKB2 HUMAN
ID FKB2 HUMAN STANDARD; PRT; 141 AA.
AC P26885;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans
isomerase) (PPIase) (EC 5.2.1.8).
GN FKB2 OR FKB13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon carcinoma;
RC MEDLINE=91319747; PubMed=1713687;
RA Jin Y.-J., Albers M.W., Lane W.S., Bierter B.E., Schreiber S.L.,
RA Burakoff S.J.;
RT "Molecular cloning of a membrane-associated human FK506- and
rapamycin-binding protein, FKBP-13."
RL Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=93112052; PubMed=1281998;
RA Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.;
RT "Chromosomal band assignments of the genes encoding human FKB12 and
FKBP13."
RL Biochem. Biophys. Res. Commun. 189:819-823 (1992).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE
ASSOCIATED (PROBABLE).
CC -!- TISSUE SPECIFICITY: T-CELLS AND THYMUS.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; M65128; AAA58473.1; -
DR EMBL; M75099; AAA36563.1; -
DR PIR; JCI365; JCI365.

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DR HSP; Q00688; LPBK.
DR Genew; HGNC:3718; FKBP2.
DR MIM; 186946; -.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
DR Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.
KW SIGNAL 1 21
FT CHAIN 22 141 FK506-BINDING PROTEIN.
FT SITE 138 141 PREVENT SECRETION FROM ER (POTENTIAL).
FT VARIANT 21 21 S -> TA.
FT VARIANT 24 24 T -> A.
FT VARIANT 96 96 /FTID=VAR_006410.
FT VARIANT 96 96 /FTID=VAR_006411.
FT VARIANT 96 96 Y -> C.
FT VARIANT 96 96 /FTID=VAR_006412.
SQ SEQUENCE 141 AA; 15654 MW; 9F4751CA7D82D064 CRC64;

Query Match 7.6%; Score 231.5; DB 1; Length 141;
Best Local Similarity 46.9%; Pred. No. 4e-10;
Matches 50; Conservative 17; Mismatches 37; Indels 3; Gaps 2;

QY 257 KQSIENKVVPCNERISQSGDPLTYHNGTLDGTLFDSSYGRNRTFDYVIGGVIP 316
DB 29 KLGIVKRV--DHCPIKSRKGDVLMHYTGKLEGTGTFDSSLPQNPQPFVPSLGTGVK 86

QY 317 GMDGGLGVGICGRXIVPPHLYGGBEGR-GNIPGSAAVLVFDIHVI 362
DB 87 GWDQGLLGYEGEKRLVIPSELGYGRGAPPKIPGGATLVFEVELL 133

RESULT 7
FKBP_NEUCR
ID FKBP_NEUCR STANDARD; PRT; 120 AA.
AC P20080;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)
DE (PPIase) (EC 5.2.1.8).
GN 966.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90348972; PubMed=1696687;
RA Tropeschug M., Wachter E., Mayer S., Schoenbrunner E.R., Schmid F.X.;
RT "Isolation and sequence of an FK506-binding protein from N. crassa
RT which catalyses protein folding."
RL Nature 346:674-677(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.-W., Mannhaupt G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506.
CC -! SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; X55743; CAA39274.1; -.
DR EMBL; AL513463; CAC28766.1; -.
DR PIR; S11090; S11090.
DR HSP; P18203; 1FKL.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 120 AA; 13037 MW; AF97183C041563B7 CRC64;

Query Match 7.5%; Score 230.5; DB 1; Length 120;
Best Local Similarity 45.0%; Pred. No. 3.9e-10;
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;

QY 31 GSDAELQIERRFVPDPCRTVRSQDFVRYHYVGTFTPDGQKQFDSSYDRDSTFNVFVGKQL 90
DB 8 GLQIEVQGE-----CQGTRETRRGDNVDVHYKGLTSGKKFDASYDRGPELNTVVGQGV 62

QY 91 ITGMDQALVGMVNERFVKIPKLAYGNRVSQVPPNSVLHFDVLLMDI 141
DB 63 IKGWDEGLLGMKIGEKRLTIAPHLAYGNRAVGVIIPANSTLIFETELVGI 113

RESULT 8
FKB4_RABIT
ID FKB4_RABIT STANDARD; PRT; 457 AA.
AC P27124;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
DE FKBP4) (EC 5.2.1.8) (PPIase) (Rotamase) (p59 protein) (HSP binding
DE immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
DE (FKBP59).
GN FKBP4 OR P59.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92165768; PubMed=1537818;
RA Lebeau M.-C., Massol N., Herrick J., Faber L.E., Renoir J.-M.,
RA Radanyi C., Baulieu E.-E.;
RT "P59, an hsp 90-binding protein. Cloning and sequencing of its cDNA
RT and preparation of a peptide-directed polyclonal antibody."
RL J. Biol. Chem. 267:4281-4284(1992).
RN [2]
RP SEQUENCE OF 1-25.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=96154240; PubMed=8579355;
RA Deshpande K.L., Seubert P.H., Tillman D.M., Parkas W.R., Katze J.R.;
RT "Cloning and characterization of cDNA encoding the rabbit
RT tRNA-guanine transglycosylase 60-kilodalton subunit."
RL Arch. Biochem. Biophys. 326:1-7(1996).
RN [3]
RP DOMAINS.
RX MEDLINE=92335279; PubMed=1631118;
RA Callebaut I., Renoir J.-M., Lebeau M.-C., Massol N., Burny A.,
RA Baulieu E.-E., Mornon J.-P.;
RT "An immunophilin that binds M(r) 90,000 heat shock protein: main
RT structural features of a mammalian p59 protein."
RL Proc. Natl. Acad. Sci. U.S.A. 89:6270-6274(1992).
RN [4]
RP PHOSPHORYLATION BY CK2.
RX MEDLINE=98070781; PubMed=9405642;
RA Miyata Y., Chambraud B., Radanyi C., Leclerc J., Lebeau M.-C.,
RA Renoir J.-M., Shirai R., Catelli M.-G., Yahara I., Baulieu E.-E.;

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"Phosphorylation of the immunosuppressant FK506-binding protein FKBP52 by casein kinase II: regulation of HSP90-binding activity of FKBP52.";  
Proc. Natl. Acad. Sci. U.S.A. 94:14500-14505(1997).

[5]  
INTERACTION WITH PHYH.  
MEDLINE=99162565; PubMed=10051602;  
Chambaud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher M.,  
Baulieu E.-E.;  
"Immunophilins, refsum disease, and lupus nephritis: the peroxisomal enzyme phytanoyl-CoA alpha-hydroxylase is a new FKBP-associated protein.";  
Proc. Natl. Acad. Sci. U.S.A. 96:2104-2109(1999).

[6]  
STRUCTURE BY NMR OF 1-148.  
MEDLINE=96374215; PubMed=8780506;  
Craescu C.T., Rouviere N., Popescu A., Cerpolini E., Lebeau M.-C.,  
Baulieu E.-E., Mispelster J.;  
"Three-dimensional structure of the immunophilin-like domain of FKBP59 in solution.";  
Biochemistry 35:11045-11052(1996).

CC -!- FUNCTION: Component of unactivated mammalian steroid receptor complexes that sediment at 8-10 S. May have a rotamase activity. May play a role in the intracellular trafficking of hetero-oligomeric forms of steroid hormone receptors.

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid hormone receptor complexes. Also interacts with peroxisomal phytanoyl-coA alpha-hydroxylase (PHYH) (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding activity.

CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.

CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.

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CC -----

DR EMBL; M84474; AAA31438.1; -

DR EMBL; M84988; AAA31439.1; -

DR PIR; A42386; A42386.

DR PDB; IKOT; 07-DEC-96.

DR PDB; IROU; 07-DEC-96.

DR InterPro; IPR001179; FKBP\_PPIase.

DR InterPro; IPR001440; TPR.

DR Pfam; PF00254; FKBP; 2.

DR Pfam; PF00515; TPR; 3.

DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.

DR PROSITE; PS00454; FKBP\_PPIASE\_2; 2.

DR PROSITE; PS00509; FKBP\_PPIASE\_3; 2.

KW Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein;

3D-structure; Phosphorylation.

FT INIT\_MET 0

FT DOMAIN 49 137 PPIASE, FKBP-TYPE 1.

FT DOMAIN 166 252 PPIASE, FKBP-TYPE 2.

FT REPEAT 269 302 TPR 1.

FT REPEAT 318 351 TPR 2.

FT REPEAT 353 385 TPR 3.

FT MOD\_RES 142 142 PHOSPHORYLATION (BY CK2).

FT CONFLICT 14 14 S -> H (IN REF. 3).

FT CONFLICT 20 21 EG -> FI (IN REF. 3).

FT CONFLICT 25 25 S -> T (IN REF. 3).

SQ SEQUENCE 457 AA; 51344 MW; EC58CC4BCF66A44A CRC64;

Query Match 7.5%; Score 228; DB 1; Length 457;

Best Local Similarity 27.5%; Pred. No. 3.2e-09;

Matches 77; Conservative 48; Mismatches 127; Indels 28; Gaps 8;

QY 139 MDIWNSEDQVQIHYFKPPSPRTIQVDFVRYHYNGFFLDGTLPDSSNNRMKTYDYTVG 198  
DB 22 VDISPKQDEGLVKVIREGTGTETPMIGDRVVFVHYTGLLDGTLKDFSSLDKDFSFGLG 81  
QY 199 IGWLI PGMDKGLLGMCVGEKRIITIPPLAYGEODGDKIPQASLVDFDVAL-----DL 253  
DB 82 KGEVIAKWDIAVATMKVGELCRITCKPEYAYGSAGSPPKIPPNATLVPEVELFEPKGBDL 141  
QY 254 HNPKDSISIEKVVENCERISQSGDFLTTHYNGTGLDGLTDFDSSYSNRRTFDT-----Y 308  
DB 142 TDDEDGGI-----RRIRTRGEGVARENDGAIVEAL--EGYKDKRLEDFQRELRE 190  
QY 309 IGQYVTP---GMDEGLLVGICIGKXIVVPPHIGYGEGRG--NIPSAVLVFIHVID 363  
DB 191 VGEISLDLPGLEKAIQRMKEGHSILYLKPSYAFNAGKEKFIIPPYAEIKVEVHLKS 250  
QY 364 FHPNPSDISITSHYKPPDCSVLSKKGD-YLKY-HYNASLL 401  
DB 251 FEKAKESWESSEKLEQSAIVKRGTVYFKGKYKQALL 290

# RESULT 9

FKB4\_HUMAN STANDARD; PRT; 458 AA.  
ID Q02790; Q9UCV7; Q9UCP1;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase  
DE FKBP4) (EC 5.2.1.8) (PPIase) (Rotamase) (p59 protein) (HSP binding  
DE immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)  
DE (FKBP59).  
GN FKBP4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Placenta;  
RX MEDLINE=93066366; PubMed=1279700;  
RA Peattie D.A., Harding M.W., Fleming M.A., Decenzo M.T.,  
RA Lippe J.A., Livingston D.J., Benasutti M.;  
RT "Expression and characterization of human FKBP52, an immunophilin  
RT that associates with the 90-kDa heat shock protein and is a component  
RT of steroid receptor complexes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:10974-10978(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, Lymph, and Uterus;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-24, SUBUNIT, AND FUNCTION.  
RC TISSUE=Thymus;  
RX MEDLINE=92285692; PubMed=1376003;  
RA Tai P.-K.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;  
RT "Association of a 59-kilodalton immunophilin with the glucocorticoid  
RT receptor complex.";  
RL Science 256:1315-1318(1992).  
RN [4]  
RP SEQUENCE OF 1-20, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.  
RC TISSUE=Lymphocytes;  
RX MEDLINE=90335211; PubMed=2378870;  
RA Sanchez E.R., Faber L.E., Henzel W.J., Pratt W.B.;  
RT "The 56-59-kilodalton protein identified in untransformed steroid  
RT receptor complexes is a unique protein that exists in cytosol in a  
RT complex with both the 70- and 90-kilodalton heat shock proteins.";  
RL Biochemistry 29:5145-5152(1990).  
RN [5]  
RP SEQUENCE OF 1-17.  
RC TISSUE=T-cell;

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RX MEDLINE=92147620; PubMed=1371107;
RA Yem A.W., Tomaselli A.G., Heinrikson R.L., Zurcher-Neely H.,
RA Ruff V.A., Johnson R.A., Deibel M.R. Jr.; complexes binds to
RT "The Hsp56 component of steroid receptor complexes binds to
RT immobilized FK506 and shows homology to FKBP-12 and FKBP-13.";
RL J. Biol. Chem. 267:2868-2871(1992).
CC -!- FUNCTION: Component of unactivated mammalian steroid receptor
CC complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of hetero-
CC oligomeric forms of steroid hormone receptors.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
CC hormone receptor complexes. Also interacts with peroxisomal
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
CC activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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DR EMBL; M88279; AAA36111.1; -
DR EMBL; BC001786; AAH01786.1; -
DR EMBL; BC002887; AAH02887.1; -
DR EMBL; BC007924; AAH07924.1; -
DR PIR; A46372; A46372.
DR HSP; P27124; IROT.
DR Genew; HGNC:3720; FKBP4.
DR MIM; 600611; -
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 2.
DR Pfam; PF00515; TPR; 3.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00453; FKBP_PPIASE 1; 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; 2.
DR PROSITE; PS00059; FKBP_PPIASE 3; 2.
DR Isomerase; Rotamase; Repeat; TPR repeat; Nuclear protein;
KW Phosphorylation.
FT INIT MET 0
FT DOMAIN 49 137 PPIASE, FKBP-TYPE 1.
FT DOMAIN 166 252 PPIASE, FKBP-TYPE 2.
FT REPEAT 269 302 TPR 1.
FT REPEAT 318 351 TPR 2.
FT REPEAT 353 385 TPR 3.
FT MOD_RES 142 142 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT CONFLICT 145 146 ED > AR (IN REF. 2; AAH02887).
FT SEQUENCE 458 AA; 51673 MW; 916B3B945C51634E CRC64;
Query Match 7.5%; Score 228; DB 1; Length 458;
Best Local Similarity 29.7%; Pred. No. 3.2e-09;
Matches 83; Conservative 35; Mismatches 115; Indels 46; Gaps 10;
QY 23 QAAPVAGLGDALQ-----IERRFVDECPRTVRSQGFVRYHYGVFPDQKEDSS 74
Db 13 QSAPLPMEGVDSIPKQDGVLVKIKREGTGTEPMI---GDRVFVHYTGWLLDGTGKFDSS 69
QY 75 YDRSTNVFVGKGLITGMDQALVGMVNERFRFKIPPKLAYGNERSVGVIPNSVLHF 134
Db 70 LDRKDKFSFDLGRKEVINKWDIATATMKVGEVCHITCKPEYAYSAGSPKIPNATLVF 129
QY 135 DVLML-----DIMNSED-----QVQIHTYKPPSCPTTIQVDFVRYHYNGTFLDGTL 182

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Db 130 EVELFEPKGBDLTEEDGGIIRIQTGEGYAKP-----NEGAIVEVALEGYKDKL 181
QY 183 FDSHNMKTYDYTVYGIGW---LIPGMDKGLGMCGVEKRIITIPPLAYGDDGDK-DI 238
Db 182 FDQRELAF-----IGEGENLDLPYGLERAIQRMKEGHSIVYLKPSVAFSGVGEKFKQI 236
QY 239 PGQASLVDFVALLDLHNPKNKSIENKVVENCERISQS 277
Db 237 PPNAELKYLHLKSFEXAKESWEMNSE-----EKLQOS 269

RESULT 10
FKBP4_MOUSE
ID FKBP4_MOUSE STANDARD; PRT; 457 AA.
AC P30416;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
DE FKBP4) (EC 5.2.1.8) (PPIase) (Rotamase) (p59 protein) (HSP binding
DE immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
DE (FKBP59).
GN FKBP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=94040772; PubMed=7693550;
RA Schmitt J., Stunnenberg H.G.;
RT "Cloning and expression of a mouse cDNA encoding p59, an immunophilin
RL Gene 132:267-271(1993).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 5-457 FROM N.A., PARTIAL SEQUENCE, FUNCTION, AND
RP SUBCELLULAR LOCATION.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=93342084; PubMed=8341706;
RA Alnemri E.S., Fernandes-Alnemri T., Nelki D.S., Dudley K.,
RA Dubois G.C., Litwack G.;
RT "Overexpression, characterization, and purification of a recombinant
RT mouse immunophilin FKBP-52 and identification of an associated
RT phosphoprotein.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6839-6843(1993).
CC -!- FUNCTION: Component of unactivated mammalian steroid receptor
CC complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of hetero-
CC oligomeric forms of steroid hormone receptors.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
CC hormone receptor complexes. Also interacts with peroxisomal
CC phytanoyl-coA alpha-hydroxylase (PHYH) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
CC activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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NCBI\_TaxID=9606;  
[1] SEQUENCE FROM N.A.  
TISSEUR=Thymus;  
MEDLINE=97242207; PubMed=9125197;  
Baughman G., Wiederrecht G.J., Chang F., Martin M.M., Bourgeois S.;  
"Tissue distribution and abundance of human FKBP51, an FK506-binding  
protein that mediate calcineurin inhibition.";  
Biochem. Biophys. Res. Commun. 232:437-443 (1997).  
[2]  
[3] SEQUENCE FROM N.A.  
Zhang J.S., Smith D.I.;  
"Identification of AIG6 as an androgen response gene in human prostate  
cancer cell line LNCap.";  
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
[5] SEQUENCE OF 9-457 FROM N.A.  
MEDLINE=97154494; PubMed=9001212;  
Nair S.C., Rimerman R.A., Toran E.J., Chen S., Prapapanich V.,  
Butts R.N., Smith D.F.;  
"Molecular cloning of human FKBP51 and comparisons of immunophilin  
interactions with Hsp90 and progesterone receptor.";  
Mol. Cell. Biol. 17:594-603 (1997).  
[6]  
[7] CHARACTERIZATION.  
MEDLINE=94043261; PubMed=7693698;  
Smith D.F., Albers M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.;  
"FKBP54, a novel FK506-binding protein in avian progesterone receptor  
complexes and Hela extracts.";  
J. Biol. Chem. 268:24270-24273 (1993).  
[8]  
[9] - FUNCTION: INTERACTS WITH FUNCTIONALLY NATURE HETERO-OLIGOMERIC  
PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.  
[10] - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
PEPTIDE BONDS IN OLIGOPEPTIDES.  
[11] - ENZYME REGULATION: INHIBITED BY FK506 BUT NOT CYCLOSPORIN.  
[12] - SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
[13] - TISSUE SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED  
TO OTHER TISSUES.  
[14] - INDUCTION: By androgen.  
[15] - SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2  
FKBP-LIKE DOMAINS.  
[16] - SIMILARITY: CONTAINS 3 TPR REPEATS.  
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EMBL; U71321; AAC51189.1; -;  
EMBL; AF1941172; AAL54872.1; -;  
EMBL; U42031; AAA86245.1; -;  
HSP; P27124; IROT.  
Genew; HGNC:3721; FKBP5.  
MIM; 602623; -;  
InterPro; IPR001179; FKBP\_PPIase.  
InterPro; IPR001440; TPR.  
Pfam; PF00254; FKBP; 2.  
Pfam; PF00515; TPR; 2.  
PROSITE; PS00453; FKBP\_PPIASE 1; 1.  
PROSITE; PS00454; FKBP\_PPIASE 2; 1.  
PROSITE; PS00059; FKBP\_PPIASE 3; 2.  
Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.  
DOMAIN 42 130 PPIASE, FKBP-TYPE 1.  
DOMAIN 157 243 PPIASE, FKBP-TYPE 2.  
REPEAT 268 301 TPR 1.  
REPEAT 317 350 TPR 2.  
REPEAT 352 384 TPR 3.  
SEQUENCE 457 AA; 51212 MW; 10A86608C6891A73 CRC64;  
Query Match 7.1%; Score 217; DR 1; Length 457;

7.18; Score 217; DB 1; Length 457;





RX MEDLINE=91126049; PubMed=1704127;  
 RA Wiederrecht G.J.; Brizuela L., Elliston K.O., Sigal N.H.,  
 RA Stekler J.J.;  
 RT "FKBP encodes a nonessential FK 506-binding protein in Saccharomyces  
 cerevisiae and contains regions suggesting homology to the  
 cyclophilins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91156723; PubMed=1705713;  
 RA Heitman J., Movva R.N., Hiestand P.C., Hall M.N.;  
 RT "FK 506-binding protein rotamase is a target for the  
 immunosuppressive agent FK 506 in Saccharomyces cerevisiae";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91141524; PubMed=1996117;  
 RA Koltin Y., Faucette L., Bergema D.J., Levy M.A., Cafferty R.,  
 RA Koser P.L., Johnson R.K., Livi G.P.;  
 RT "Rapamycin sensitivity in Saccharomyces cerevisiae is mediated by a  
 peptidyl-prolyl cis-trans isomerase related to human FK506-binding  
 protein.";  
 RL Mol. Cell. Biol. 11:1718-1723(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=S288C;  
 RA Mallet L., Bussereau F., Jacquet M.;  
 RT "A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,  
 MFA2, CAP/SRV2, NAM9, FKBP1/FRP1, MCM22 and CPT1, predicts an  
 adenosine deaminase gene and 14 new open reading frames.";  
 RL Yeast 11:1195-1209(1995).  
 RN [5]  
 RP SEQUENCE OF 67-100.  
 RX MEDLINE=91065908; PubMed=1701173;  
 RA Stekler J.J., Widerrecht G., Gzeulich H., Boulton D., Hung S.H.Y.,  
 RA Cryan J., Hodges P.J., Sigal N.H.;  
 RT "The cytosolic-binding protein for the immunosuppressant FK-506 is  
 both a ubiquitous and highly conserved peptidyl-prolyl cis-trans  
 isomerase.";  
 RL J. Biol. Chem. 265:21011-21015(1990).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=93216714; PubMed=7681823;  
 RA Roconda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;  
 RT "Improved calcineurin inhibition by yeast FKBP12-drug complexes.  
 Crystallographic and functional analysis.";  
 RL J. Biol. Chem. 268:7607-7609(1993).  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND  
 ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC  
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 CC  
 DR EMBL; Z46843; CAA86890.1; -;  
 DR EMBL; M57967; AAA03564.1; -;  
 DR EMBL; M60877; AAA34607.1; -;  
 DR EMBL; M63892; AAA34962.1; -;  
 DR EMBL; Z71411; CAA96017.1; -;  
 DR PIR; A33146; A33146.  
 DR PIR; A37870; A37870.  
 DR PIR; A39122; A39122.  
 DR PIR; C38333; C38333.

DR PIR; S13758; S13758.  
 DR DB; 1YAT; 31-OCT-93.  
 DR SGD; S0005079; FPR1.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR Pfam; PF00254; FKBP; 1.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE; PS00059; FKBP\_PPIASE\_3; 1.  
 KW Isomerase; Rotamase; 3D-structure.  
 FT STRAND 3 4  
 FT HELIX 6 8  
 FT STRAND 10 15  
 FT TURN 25 26  
 FT STRAND 28 37  
 FT TURN 38 39  
 FT STRAND 42 45  
 FT TURN 47 50  
 FT STRAND 53 56  
 FT TURN 57 58  
 FT HELIX 64 72  
 FT TURN 75 76  
 FT STRAND 78 83  
 FT HELIX 85 87  
 FT TURN 88 92  
 FT STRAND 94 97  
 FT TURN 95 98  
 FT STRAND 100 101  
 FT STRAND 104 113  
 SQ SEQUENCE 114 AA; 1215 MW; 65C134830D300C06 CRC64;  
 Query Match 6.8%; Score 207; DB 1; Length 114;  
 Best Local Similarity 43.8%; Pred. No. 1.8e-08;  
 Matches 44; Conservative 13; Mismatches 44; Indels 0; Gaps 0;  
 QY 41 RFVDECPRTVRSQDFVRYHYVGFDPQKQFDSYDSTFNFGKGLITGMDQALVG 100  
 Db 13 RISPGDGTGPKGDLVTIHYTGLENGKQFDSYDSTFNFGKGLITGMDQALVG 72  
 QY 101 MCVNERFVKIPKLAAYGNERSGVIPNPSVLFHFDVLMDI 141  
 Db 73 LSVGEKARLTIPGYPAYGPRGPGIIPNSTLVDFVLLKV 113  
 RESULT 14  
 FKBP\_SCHPO  
 ID -FKBP\_SCHPO STANDARD; PRT; 112 AA.  
 AC 042993;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)  
 DE (PPIase) (EC 5.2.1.8).  
 GN SPC24E9.17C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=91848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell E.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

```
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritsch C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; AL096796; CAB46710.1; -
DR HSSP; P20081; IYAT.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 112 AA; 12043 MW; 355944ECB84D2539 CRC64;

Query Match 6.4%; Score 196; DB 1; Length 112;
Best Local Similarity 45.6%; Pred. No. 1.1e-07;
Matches 41; Conservative 12; Mismatches 37; Indels 0; Gaps 0;

QY 52 RSGDFVRYHYVCTPFGQKSSYDRDSTFNVFVGKGLITGMDQALVGMCVNRRFVKI 111
DB 18 KPGDRITMHTYGTLTNGKKDSSVDKSPFVCTTIGVQGLIRGWDKGVKMSLGEKAKLTI 77

QY 112 PPKLAYGNVRSVGIIPNPNVLFHFDVLLMDI 141
DB 78 TPDYGYGPRGPGGLIPNSTLLFVLLAI 107

RESULT 15
ID_FKBP1 DROME STANDARD; PRT; 108 AA.
AC P48375;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 12 kDa FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Macrolide binding protein).
GN FK506-BP2 OR FKBP12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S; TISSUE=Head;
```

```
RA Mounsey A.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
RA Lechleider R.J., Martin J., Manganaro T., Donahoe P.K.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49079; CAA88904.1; -
DR EMBL; U41441; AAR11178.1; -
DR HSSP; P18203; IFKL.
DR FlyBase; FBgn0013954; FK506-bp2.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 108 AA; 11597 MW; 48BCF993AC8D350A CRC64;

Query Match 6.4%; Score 195.5; DB 1; Length 108;
Best Local Similarity 36.1%; Pred. No. 1.1e-07;
Matches 43; Conservative 16; Mismatches 45; Indels 15; Gaps 1;

QY 23 QAAPVAGLGSDAELQIERRFVDECPRTVRSQDGFVRYHYVGTFFDGQKFDSSYDRDSTFN 82
DB 4 QVVPIA-----FQDGGSTYKNGQKVTVHYTGTLLDGTGTFDSSRDNRKPFK 48

QY 83 VFGVGKGLITGMDQALVGMCVNRRFVKIIPKLAYGNVRSVGIIPNPNVLFHFDVLLMDI 141
DB 49 FTIGKGEVIRGWDEGVAGLQSVGSAKLICSPDYVAGSRGHPGVIPNPNSTLTDFVLLKV 107

Search completed: April 26, 2003, 06:56:20
Job time : 12.2323 secs
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GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 50.5014 Seconds  
(without alignments)  
2341.934 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAPRGWRPPPPPLLLLLLW.....AEEFLXQBAKHVDVTLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.\*

1: sp archaea.\*

2: sp bacteria.\*

3: sp fungi.\*

4: sp human.\*

5: sp invertebrate.\*

6: sp mammal.\*

7: sp mhc.\*

8: sp organelle.\*

9: sp phage.\*

10: sp plant.\*

11: sp rodent.\*

12: sp virus.\*

13: sp vertebrate.\*

14: sp unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID        | Description        |
|------------|--------|-------------|--------|-----------|--------------------|
| 1          | 2805   | 91.8        | 570    | 11 Q8R386 | Q8r386 mus musculu |
| 2          | 2796   | 91.6        | 570    | 11 Q9Z247 | Q9z247 mus musculu |
| 3          | 2723   | 89.2        | 517    | 4 Q95302  | Q95302 homo sapien |
| 4          | 2380.5 | 77.9        | 577    | 13 Q9YIC3 | Q9yic3 gallus gall |
| 5          | 1772   | 58.0        | 564    | 13 Q9I8P8 | Q9i8p8 xenopus lae |
| 6          | 1753.5 | 57.4        | 581    | 11 Q8VHI1 | Q8vhi1 mus musculu |
| 7          | 1744   | 57.1        | 582    | 4 Q9H3N3  | Q9h3n3 homo sapien |
| 8          | 1742   | 57.0        | 582    | 4 Q96AY3  | Q96ay3 homo sapien |
| 9          | 1522   | 49.8        | 481    | 4 Q9H6N5  | Q9h6n5 homo sapien |
| 10         | 845.5  | 27.7        | 355    | 4 Q9H6J3  | Q9h6j3 homo sapien |
| 11         | 736    | 24.1        | 262    | 4 Q9UF89  | Q9uf89 homo sapien |
| 12         | 464.5  | 15.2        | 137    | 13 Q98UD7 | Q98ud7 xenopus lae |
| 13         | 344.5  | 11.3        | 261    | 5 Q16309  | Q16309 caenorhabdi |
| 14         | 343    | 11.2        | 264    | 5 P91180  | P91180 caenorhabdi |
| 15         | 343    | 11.2        | 300    | 5 Q95Q60  | Q95q60 caenorhabdi |
| 16         | 338.5  | 11.1        | 578    | 10 Q9FJL3 | Q9fjl3 arabidopsis |

|    |       |      |     |           |                    |
|----|-------|------|-----|-----------|--------------------|
| 17 | 311   | 10.2 | 551 | 10 Q38931 | Q38931 arabidopsis |
| 18 | 311   | 10.2 | 551 | 10 Q38949 | Q38949 arabidopsis |
| 19 | 311   | 10.2 | 555 | 10 Q9LSF3 | Q9lsf3 arabidopsis |
| 20 | 309   | 10.1 | 216 | 5 Q9V3V2  | Q9v3v2 drosophila  |
| 21 | 307   | 10.1 | 216 | 5 Q9XZ54  | Q9xz54 drosophila  |
| 22 | 307   | 10.1 | 568 | 10 Q04843 | Q04843 triticum ae |
| 23 | 294.5 | 9.6  | 259 | 5 Q23338  | Q23338 caenorhabdi |
| 24 | 286.5 | 9.4  | 139 | 5 Q20107  | Q20107 caenorhabdi |
| 25 | 270   | 8.8  | 138 | 5 Q9VGK3  | Q9vgk3 drosophila  |
| 26 | 268   | 8.8  | 222 | 4 Q9Y6B0  | Q9y6b0 homo sapien |
| 27 | 268   | 8.8  | 222 | 4 Q96DA4  | Q96da4 homo sapien |
| 28 | 267.5 | 8.8  | 209 | 5 Q966Y5  | Q966y5 suberites d |
| 29 | 263.5 | 8.6  | 312 | 2 Q53919  | Q53919 streptomyce |
| 30 | 263   | 8.6  | 151 | 10 Q41649 | Q41649 vicia faba  |
| 31 | 262.5 | 8.6  | 304 | 5 Q9XW05  | Q9xw05 caenorhabdi |
| 32 | 259.5 | 8.5  | 163 | 10 Q9FJL2 | Q9fjl2 arabidopsis |
| 33 | 259.5 | 8.5  | 163 | 10 Q38936 | Q38936 arabidopsis |
| 34 | 256   | 8.4  | 211 | 4 Q9NWM8  | Q9nmw8 homo sapien |
| 35 | 256   | 8.4  | 218 | 11 Q54998 | Q54998 mus musculu |
| 36 | 254.5 | 8.3  | 134 | 5 Q17280  | Q17280 botryllus s |
| 37 | 253.5 | 8.3  | 589 | 10 Q94J55 | Q94j55 oryza sativ |
| 38 | 253   | 8.3  | 146 | 10 Q38935 | Q38935 arabidopsis |
| 39 | 253   | 8.3  | 153 | 10 Q9LSF4 | Q9lsf4 arabidopsis |
| 40 | 249.5 | 8.2  | 259 | 4 Q9Y680  | Q9y680 homo sapien |
| 41 | 242.5 | 7.9  | 142 | 4 Q9BTS7  | Q9bts7 homo sapien |
| 42 | 231.5 | 7.6  | 137 | 5 Q96335  | Q96335 brugia mala |
| 43 | 226   | 7.4  | 439 | 5 Q9U4N1  | Q9u4n1 drosophila  |
| 44 | 225.5 | 7.4  | 152 | 5 Q8T109  | Q8t109 bombyx mori |
| 45 | 225   | 7.4  | 439 | 5 Q9VL78  | Q9vl78 drosophila  |

## ALIGNMENTS

RESULT 1

Q8R386 ID Q8R386 PRELIMINARY; PRT; 570 AA.  
AC Q8R386;  
DT 01-JUN-2002 (TREMELrel. 21, Created)  
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)  
DE FK506 binding protein 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC026133; AAH26133.1; --  
SQ SEQUENCE 570 AA; 63014 MW; 06AB7BD18786B9D5 CRC64;

Query Match 91.8%; Score 2805; DB 11; Length 570;  
Best Local Similarity 93.1%; Pred. No. 3.5e-215;  
Matches 526; Conservative 15; Mismatches 22; Indels 2; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| QY | 4   | RGWRPPPPPLLLLLLWTGQAAPVAGLGSDAEIQIERRFVDPDECPRTVRSQDFVRYHYVG   | 63  |
| DB | 6   | RGWR--RRSLLLLLLWTGQAAPVLGLAVSSSELQIQRSFVDPDECPRTVHSGDFVRYHYVG  | 63  |
| QY | 64  | TFPDGOKFSSYDRDSTFNFGKGLITGMDQALVGMVCNERRFVKTPPKLAVGNERSV       | 123 |
| DB | 64  | TFLDGQKFDSSYDRDSTFNFGKGLITGMDQALVGMVCNERRLVTIPPNLAYSGSGVS      | 123 |
| QY | 124 | GVIPPNVSLHFDVLLDMNSEDQVQIHTYFKPSPCPTIQVDFVRYHYNGTFLDGLTF       | 183 |
| DB | 124 | GVIPPNVSLHFDVLLDMNSEDQVQIHTYFKPSPCPTIQVDFVRYHYNGTFLDGLTF       | 183 |
| QY | 184 | DSSHNRMKTYDVTYVGIGWLIPGMDKGLLGMVCVGEKRIITIPPFLLAYBGDGGKQIPGQAS | 243 |
| DB | 184 | DSSHNRMKTYDVTYVGIGWLIPGMDKGLLGMVCVGEKRIITIPPFLLAYBGDGGKQIPGQAS | 243 |

QY 244 LVFDVALLDHPKDSISIKNVKVPENCERISQSGDELTYHYNGTLLDGTLPDSSYSRNR 303  
 DB 244 LVFDVALLDHPKDSISIKNVKVPENCERISQSGDELTYHYNGTLLDGTLPDSSYSRNRH 303  
 QY 304 TFDYIIGQYVPGWDEGLLGVICIGKRXIVPPHLYGEGEGRNIPGSAVLFDIHDVID 363  
 DB 304 TFDYIIGQYVPGWDEGLLGVICIGKRXIVPPHLYGEGEGRNIPGSAVLFDIHDVID 363  
 QY 364 FHPSPDSISITSHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGS 423  
 DB 364 FHPSPDSISITSHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGS 423  
 QY 424 QVVLGMDMGLRECMVCGKRTVIIIPHLGYGAGVDGVEPGSAVLFDIEXLVLVAGLPRG 483  
 DB 424 QVVLGMDMGLRECMVCGKRTVIIIPHLGYGAGVDGVEPGSAVLFDIEXLVLVAGLPRG 483  
 QY 484 YPMIWNGEVSPNLFEEIDKGNVGLLEEFSEYIHAQVAGSKGLAPGDAELIVKNMFT 543  
 DB 484 YPMIWNGEVSPNLFEEIDKGNVGLLEEFSEYIHAQVAGSKGLAPGDAELIVKNMFT 543  
 QY 544 NDRNGDGKVTAEFKLXDOEAKHD 568  
 DB 544 NDRNGDGKVTAEFKLXDOEAKHD 568 36

RESULT 2  
 Q92247 PRELIMINARY; PRT; 570 AA.  
 AC Q92247 Q9JHX5; Q9CVM0;  
 DT 01-MAY-1999 (T-REMBLrel. 10, Created)  
 DT 01-MAY-1999 (T-REMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (T-REMBLrel. 20, Last annotation update)  
 DE FK506 binding protein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (TKBP65RS).  
 GN FKBP9 OR FKBP63.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., ENZYME REGULATION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND CALCIUM-BINDING ACTIVITY.  
 RX MEDLINE=99453729; PubMed=10524204;  
 RA Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krause S.;  
 RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP family";  
 RL Biochim. Biophys. Acta 1446:295-307(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=THYMUS;  
 RX PubMed=11710534;  
 RA Jo D., Iyu M.S., Cho E.-G., Park D., Kozak C.A., Kim M.G.;  
 RT "Identification and genetic mapping of the mouse Fkbp9 gene encoding a new member of FK506-binding protein family";  
 RL Mol. Cells 12:272-275(2001).  
 RN [3]  
 RP SEQUENCE OF 155-570 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gassner T., Giesi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
 RA Bownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,  
 RA Gustincich S., Hill D., Hofmann M., Fujita M., Gariboldi M.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kamiya M., Lee N.H.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayaashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001)  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING PROTEIN SYNTHESIS.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- ENZYME REGULATION: INHIBITED BY FK506.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.  
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL MUSCLE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN, SPLEEN AND TESTIS.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL DEVELOPMENTAL STAGES.  
 CC -!- PTM: PHOSPHORYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 CC EMBL; AF090334; AAC72964.1; -;  
 DR EMBL; AF279263; AAF79215.1; -;  
 DR EMBL; AK007499; BAB25071.1; -;  
 DR HSSP; P20081; 1YAT.  
 DR MGD; MGI:1350921; Fkbp9.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR Pfam; PF00036; efhand; 2.  
 DR Pfam; PF00254; FKBP; 4.  
 DR SMART; SM00054; Eph; 2.  
 DR PROSITE; PS00018; EF\_HAND; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00453; FKBP\_PPIASE 1; FALSE\_NEG.  
 DR PROSITE; PS00454; FKBP\_PPIASE 2; 3.  
 DR PROSITE; PS00455; FKBP\_PPIASE 3; 4.  
 DR PROSITE; PS50059; FKBP\_PPIASE 3; 4.  
 KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 570 FK506 BINDING PROTEIN 9.  
 FT DOMAIN 45 139 PPIASE, FKBP-TYPE 1.  
 FT DOMAIN 158 251 PPIASE, FKBP-TYPE 2.  
 FT DOMAIN 269 362 PPIASE, FKBP-TYPE 3.  
 FT DOMAIN 381 474 PPIASE, FKBP-TYPE 4.  
 FT CA\_BIND 492 520 PPIASE, FKBP-TYPE 4.  
 FT CA\_BIND 537 563 EF-HAND 2 (POTENTIAL).  
 FT SITE 567 570 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 234 236 DGK -> NGE (IN REF. 2).  
 FT CONFLICT 321 321 G -> S (IN REF. 3).  
 FT CONFLICT 351 351 G -> A (IN REF. 2).  
 FT CONFLICT 353 353 A -> T (IN REF. 3).  
 FT CONFLICT 361 361 V -> F (IN REF. 2).  
 FT CONFLICT 364 364 F -> V (IN REF. 2).  
 FT CONFLICT 378 378 K -> N (IN REF. 2).  
 FT CONFLICT 386 386 S -> I (IN REF. 2).  
 FT CONFLICT 475 475 E -> D (IN REF. 2).  
 FT CONFLICT 550 550 D -> N (IN REF. 2).  
 SQ SEQUENCE 570 AA; 62995 MW; DFE8B8F2F6A0FIDA CRC64;  
 Query Match 91.6%; Score 2796; DB 11; Length 570;  
 Best Local Similarity 92.7%; Pred. No. 1.9e-214;  
 Matches 524; Conservative 16; Mismatches 23; Indels 2; Gaps 1;  
 QY 4 RGRPPPPPLLLLLLWVTGQAAPVAGLSDAELQIERFVDECPRTVRSQGFVRYHYVG 63  
 DB 6 RGR--RRSLLLLLWVTGQAAPVGLAVSELQIQSFVDECPRTVHSQGFVRYHYVG 63  
 QY 64 TFPDQKGFSSYDRDSTFNVFVGKQLITGMQDALVGMVNERFVKLPKPLAYNERVS 123

Db 64 TFLDQKFDSSYDRDSTFNVVGKQLIAGMDQALVGMVNERELVTIPPNLAYSGEVS 123  
 QY 124 GVTPPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTQVSDVFRHYHNGTFLDGTLP 183  
 Db 124 GVTPPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTQVSDVFRHYHNGTFLDGTLP 183  
 QY 184 DSSHNRKMTYDVTYVGLGWLIPGMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPGQAS 243  
 Db 184 DSSHNRKMTYDVTYVGLGWLIPGMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPGQAS 243  
 QY 244 LVFDVALLDLHNPKDSISIEKVVPPENCERISQSGDFTLYHNGTLLDGTFLDSSYSNR 303  
 Db 244 LVFDVALLDLHNPKDSISIEKVVPPENCERISQSGDFTLYHNGTLLDGTFLDSSYSNR 303  
 QY 304 TFDYTIQGGVIVPGMDGLGVCIGERRIVVPPHLYGEGRGSGIPGSAVLVDFDIHVID 363  
 Db 304 TFDYTIQGGVIVPGMDGLGVCIGERRIVVPPHLYGEGRGSGIPGSAVLVDFDIHVID 363  
 QY 364 FHNPSDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGLDSTWNLTGTYNIVLGS 423  
 Db 364 FHNPSDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGLDSTWNLTGTYNIVLGS 423  
 QY 424 QVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGEVPGSAVLVDFIEXLELVAGLPEG 483  
 Db 424 QVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGEVPGSAVLVDFIEXLELVAGLPEG 483  
 QY 484 YMFIVNGEVSPLFEEDKDGNGEVLLEEFSEYTHAQVASKGKLAPGFAELIVKNNFT 543  
 Db 484 YMFIVNGEVSPLFEEDKDGNGEVLLEEFSEYTHAQVASKGKLAPGFAELIVKNNFT 543  
 QY 544 NQDRNGDGKVTAEFKLKDQAKHD 568  
 Db 544 NQDRNGDGKVTAEFKLKDQAKHD 568

RESULT 3  
 095302 PRELIMINARY; PRT; 517 AA.  
 AC 095302; 0961J9; 096X5;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE FK506 binding protein 9 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (Fragment).  
 GN FKBP9 OR FKBP63.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99453729; PubMed=10524204;  
 RA Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;  
 RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP family";  
 RL Biochim. Biophys. Acta 1446:295-307(1999).  
 RN [2]  
 RP SEQUENCE OF 317-517 FROM N.A.  
 RC TISSUE=KIDNEY, AND MUSCLE;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING PROTEIN SYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- ENZYME REGULATION: INHIBITED BY FK506 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (BY SIMILARITY).  
 CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 DR EMBL; AF089745; AAC78853.1; -.  
 DR EMBL; BC007443; AAH07443.1; -.

DR EMBL; BC011872; AAH11872.1; -.  
 DR HSSP; P20081; 1YAT  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR Pfam; PF00036; ehand; 2.  
 DR Pfam; PF00254; FKBP; 4.  
 DR SMART; SM00054; EFh; 2.  
 DR PROSITE; PS00018; EF\_HAND; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 3.  
 DR PROSITE; PS00509; FKBP\_PPIASE\_3; 4.  
 KW Isomerase; Rotamase; Repeat; Glycoprotein; Phosphorylation; Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 86 PPIASE, FKBP-TYPE 1.  
 FT DOMAIN 105 198 PPIASE, FKBP-TYPE 2.  
 FT DOMAIN 216 309 PPIASE, FKBP-TYPE 3.  
 FT DOMAIN 328 421 PPIASE, FKBP-TYPE 4.  
 FT CA\_BIND 439 467 EF-HAND 1 (POTENTIAL).  
 FT CA\_BIND 484 510 EF-HAND 2 (POTENTIAL).  
 FT SITE 514 517 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 317 319 SIS -> HEG (IN REF. 2; AAH07443).  
 FT CONFLICT 514 514 H -> Q (IN REF. 2; AAH11872).  
 SQ SEQUENCE 517 AA; 57219 MW; 704F80CE9C4C74B CRC64;  
 Query Match 89.2%; Score 2723; DB 4; Length 517;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-208; Indels 0; Gaps 0;  
 Matches 510; Conservative 0; Mismatches 5;  
 QY 54 GDFVRYHYVGTFFDQKFDSSYDRDSTFNVVGKQLITGMDQALVGMVNERELVTIPPN 113  
 Db 1 GDFVRYHYVGTFFDQKFDSSYDRDSTFNVVGKQLITGMDQALVGMVNERELVTIPPN 60  
 QY 114 KLAYGNRVSQVVPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTQVSDVFRHY 173  
 Db 61 KLAYGNRVSQVVPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTQVSDVFRHY 120  
 QY 174 NGTFDGLTFLDSSHNRKMTYDVTYVGLGWLIPGMDKGLGMCVGEKRIITPPFLAYGEDG 233  
 Db 121 NGTFDGLTFLDSSHNRKMTYDVTYVGLGWLIPGMDKGLGMCVGEKRIITPPFLAYGEDG 180  
 QY 234 DGKDIPGQASLVFDVALLDLHNPKDSISIEKVVPPENCERISQSGDFTLYHNGTLLDGT 293  
 Db 181 DGKDIPGQASLVFDVALLDLHNPKDSISIEKVVPPENCERISQSGDFTLYHNGTLLDGT 240  
 QY 294 LFDSSYSNRRTFTYTIQGGVIVPGMDGLGVCIGERRIVVPPHLYGEGRGSGIPGSA 353  
 Db 241 LFDSSYSNRRTFTYTIQGGVIVPGMDGLGVCIGERRIVVPPHLYGEGRGSGIPGSA 300  
 QY 354 VLVFDLHVDFDHNPSDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGLDSTWNLTG 413  
 Db 301 VLVFDLHVDFDHNPSDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGLDSTWNLTG 360  
 QY 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGEVPGSAVLVDFDIEX 473  
 Db 361 KTYNIVLGSQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGEVPGSAVLVDFDIEX 420  
 QY 474 LELVAGLPEGYMFIVNGEVSPLFEEDKDGNGEVLLEEFSEYTHAQVASKGKLAPGFD 533  
 Db 421 LELVAGLPEGYMFIVNGEVSPLFEEDKDGNGEVLLEEFSEYTHAQVASKGKLAPGFD 480  
 QY 534 AELIVKNNFTNQDRNGDGKVTAEFKLKDQAKHD 568  
 Db 481 AELIVKNNFTNQDRNGDGKVTAEFKLKDQAKHD 515  
 RESULT 4

## Q9YIC3

ID Q9YIC3 PRELIMINARY; PRT; 577 AA.  
AC Q9YIC3  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE CFBP/SMAP.  
GN CFBP/SMAP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98384310; PubMed=9716519;  
RA Fukuda K., Tanigawa Y., Fujii G., Yasugi S., Hirohashi S.;  
RT "cFBP/SMAP; a novel molecule involved in the regulation of smooth  
muscle differentiation.";  
RL Development 125:3535-3542(1998).  
DR EMBL; AB008675; BAA34673.2; -.  
DR HSP; P27124; 1R0T.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000886; ER-target.  
DR InterPro; IPR001179; FKBP\_PPase.  
DR Pfam; PF00036; ehand; 2.  
DR Pfam; PF00254; FKBP; 4.  
DR SMART; SM00054; EPH; 2.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00454; FKBP\_PPASE\_2; UNKNOWN\_3.  
DR PROSITE; PS00059; FKBP\_PPASE\_3; 4.  
SQ SEQUENCE 577 AA; 64054 MW; 1E85DEA387AE099B CRC64;

Query Match 77.9%; Score 2380.5; DB 13; Length 577;  
Best Local Similarity 78.6%; Pred. No. 2.6e-181;  
Matches 442; Conservative 54; Mismatches 55; Indels 11; Gaps 4;

QY 15 LLLLLWVTAQAPVAGL---GSDAELQIERFVDECPRTVRSQDFVRYHYVGFDPGQKF 71  
DB 17 LLSVNAACQAPPVAAEPWGDADVHVERFVPERLPRVRRGDFVRYHYLGFDPGTRF 76  
QY 72 DSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNERSVGVPNSV 131  
DB 77 DSSYDRGSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYSGSGVPIPNV 136  
QY 132 LHFVLLMDIWNSEDQVQIHTVFKPPCPRTIQVSDFVRYHYNGTFLDGTLPDSSSHNMK 191  
DB 137 LHFVLLMDIWNSEDEVQVETVFKPKCTRRVQVSDFVRYHYNGTFLDGTLPDSSSHNM 196  
QY 192 TYDTYVIGLWIPGMKGLLGMVCGEKRIITIPPELAYGSDGKDI PGQASLVFDVALL 251  
DB 197 TYDTYVIGLWIPGMKGLLGMVCGEKRIITIPPELAYGSDGKDI PGQASLVFDVALL 256  
QY 252 DLHNPDSISIKNVVPCERISQSGDFTLYHYNGTLLDGTLPDSSSYNRNFTDYIGQ 311  
DB 257 DLHNPDKGITTENQLVPESCERRTQGDFTYHYNGTLLDGTLPDSSSYNRNFTDYIGQ 316  
QY 312 GVIIPGMDGLLGVCI GKKXIVVPHLGYGEGRGNIPGSALVFDIHDVDFHNPDSI 371  
DB 317 GVIIPGMDGLLGVCI GKKXIVVPHLGYGEGRGNIPGSALVFDIHDVDFHNPDSI 376  
QY 372 SITSHYKPPDCSVLSKKGDKYKHYNASLTI---DGTLLDSTWNLGKTYNVLGSGQVVLG 428  
DB 377 SITVNYKPSNCSLLSKGDKYKHYNASLTI---DGTLLDSTWNLGKTYNVLGSGQVVLG 433  
QY 429 MDMLREMCVGEKRTVIIIPPHLGYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMF 488  
DB 434 MDMLQDMCVGERRTIIIPPHLGYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMF 493  
QY 489 NGEVSPNLFEEIDKNGGVLLREFSEYTHA VASCKGLACGFDAELIVKNNFTNQDRN 548  
DB 494 NGEVSPNLFEEIDQNHGDEVLLEEFSEYTHA VASCKGLACGFDAELIVKNNFTNQDRN 553

QY 549 GDGKVTAEEFKLXQDEAK--HD 568  
DB 554 GNGKVTAEEFKLXQDEAKGHD 575

## RESULT 5

Q918P8  
ID Q918P8 PRELIMINARY; PRT; 564 AA.  
AC Q918P8  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE FK506-binding protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20302564; PubMed=10842073;  
RA Spokony R., Saint-Jeannet J.-P.;  
RT "Xenopus FK 506-binding protein, a novel immunophilin expressed during  
early development.";  
RL Mech. Dev. 94:205-208(2000).  
DR EMBL; AF232672; AAF35906.1; -.  
DR HSP; P20081; 1YAT.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000886; ER-target.  
DR InterPro; IPR001179; FKBP\_PPase.  
DR Pfam; PF00036; ehand; 2.  
DR Pfam; PF00254; FKBP; 4.  
DR SMART; SM00054; EPH; 2.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00454; FKBP\_PPASE\_2; UNKNOWN\_2.  
DR PROSITE; PS00059; FKBP\_PPASE\_3; 4.  
SQ SEQUENCE 564 AA; 62643 MW; 15312365BF1E43CF CRC64;

Query Match 58.0%; Score 1772; DB 13; Length 564;  
Best Local Similarity 59.5%; Pred. No. 8.5e-133;  
Matches 329; Conservative 82; Mismatches 134; Indels 8; Gaps 3;

QY 13 LLLLLWVTAQAPVAGLSDAELQIERFVDECPRTVRSQDFVRYHYVGFDPGQKF 72  
DB 10 LHFVLLVACDSGL-----EDVVIDRYDIPKICPREVQMGDFVRYHYNGTFFDQKQF 63  
QY 73 SSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNERSVGVPNSV 132  
DB 64 ASYDRGVAVAGFVGVRGLITGLDRGILGMVNEKRLIVPPHPLGYGSGVPGMIPADATL 123  
QY 133 HFDVLLMDIWNSEDQVQIHTVFKPPCPRTIQVSDFVRYHYNGTFLDGTLPDSSSHNMKT 192  
DB 124 YFDILLQDIWNKDEVOITTIHKASPCNRSVQSDDFVRYHYNGTLLDGTLPDSSSYRSTT 183  
QY 193 YDTYVIGLWIPGMKGLLGMVCGEKRIITIPPELAYGSDGKDI PGQASLVFDVALL 252  
DB 184 YDTYVIGLWIPGMKGLLGMVCGEKRIITIPPELAYGSDGKDI PGQASLVFDVALL 243  
QY 253 LHNPKDISIKNVVPCERISQSGDFTLYHYNGTLLDGTLPDSSSYNRNFTDYIGQ 312  
DB 244 FHNPKDITVQNVQVPCRRKAVGIDYVRYHYNGTLLDGTLPDSSSYNRNFTDYIGQ 303  
QY 313 YVTPGMDGLLGVCI GKKXIVVPHLGYGEGRGNIPGSALVFDIHDVDFHNPDSI 371  
DB 304 YVTPGMDGLLGVCI GKKXIVVPHLGYGEGRGNIPGSALVFDIHDVDFHNPDSI 363  
QY 372 SITSHYKPPDCSVLSKKGDKYKHYNASLTDGTLTWNLGKTYNVLGSGQVVLGMDM 431  
DB 364 DIEVMKPDSCNTTSKKGDFIKHYNCMLDGTLLFFSHEYETPQQVTGLSSKVIETGLT 423  
QY 432 GLREMCVGEKRTVIIIPPHLGYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMF 491



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Db 424 GLLCMVGERTVDPVPHLAGHSGARG-VPPSAVLAFDLELLHIERGIPGCVLFIWLD 482
QY 492 VSNLFEIDKNGEVLLEEFSEYIIHAQVAGSGKGLAPGDAELIVKNMFTNQDRNGDG 551
Db 483 TPNELFEIMDLKNGEVPPEBFDLKAQVSEKGRFLPGVDREKSTADMEVNDNRKDG 542
QY 552 KVTAEEFKLXDOE 564
Db 543 KITADELKLKTEE 555

RESULT 6
Q8VH11 PRELIMINARY; PRT; 581 AA.
AC Q8VH11;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65 kDa FK506-binding protein.
GN FKBP10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Patterson C.E., Gao J., Rooney A.P., Davis E.C.;
RT "Genomic Organization of Mouse and Human 65 kDa FK506-binding protein
RT (FKBP65) Genes and Evolution of the FKBP Multigene Family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF456413; AAL57621.1; JOINED.
DR EMBL; AF456412; AAL57621.1; JOINED.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 581 AA; 64697 MW; FD6F77940AD91E9 CRC64;

Query Match 57.4%; Score 1753.5; DB 11; Length 581;
Best Local Similarity 58.9%; Pred. No. 2.6e-131;
Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY 12 PLILLILLVW---TQAPAVAGLGSDAELQIERFVDPCEPTRVSGDFVRHYVGTFFDG 68
Db 18 PLILLQLTERGLGRASP-AGAPLE-DVIERHYHIPRACPREVQMGDFVRHYNGTFEDG 75
QY 69 QKPDSSYDRSTFNVFVGKGLITGMDOALVGMCVNERFVKIPKLAGNERVSGVIPP 128
Db 76 KXPDSSYDRSTLVAIVVGRLITGMDOALVGMCVNERRLIVPHLGVSGIVAGLAPP 135
QY 129 NSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRHYNGTFLDGTLPDSSHN 188
Db 136 DATLYDFVLLDVNWKADTVQSTILLRPYCPRMVQNSDFVRHYNGTLLDGTAFDNSYS 195
QY 189 RMKTYDTVVGILPGMDKGLGNCVGEKRIITIPPLAYGEDGDGKDIPOQASLVFV 248
Db 196 RGGTYDTYIGSGWIKGMDQGLGNCVGEKRIITIPPLAYGEKGYGTVIPQASLVFV 255
QY 249 ALLDLHNPKDISIENKVVPCNERISQSGDPLTYHYNGTLLDGTLPDSSYSRNETFDY 308
Db 256 LLLDVHNPQDTVQLETLELPQCVRRAVAGDPMRHYNGSLMDGTLPDSSYSRNETYNTY 315
QY 309 IQGGYVITPGMDEGLGVGICGKRKXIVVPHLGVGEGEGRN-IPGSAVLVFDLHVDFHNP 367
Db 316 VQGGYIIPGMDDQGLGACIGERRRITVPPHAYGNGTGDKIPGSAVLIFDVHVIDFHP 375

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QY 368 SDSISITSHYKPPD-CSVLSSKGDYLYHYNASLDDGTLLDSTWNLGKTYNIVLSSGOV 426
Db 376 SDPVEIKTLRSRPENCNFTSKIGDFIRHYNCSLDGTGLFSGSHOYEAPOEITLGANKVI 435
QY 427 LGMDMLGEMCVGKERTVITIPHLGVGEAGVDGVPGSVAVLFDIEKLELVAGLPGGYMF 486
Db 436 EGLDRGLQCMVGERRQLIVPHLAHGENGARG-VPGSAVLLEFEVLVSREDGLPTGYLP 494
QY 487 IWNGEVSNLFEIDKNGEVLLEEFSEYIIHAQVAGSGKGLAPGDAELIVKNMFTNQD 546
Db 495 VVYQDPSTSLFEDMDLNKDGVEPPPEBFSFIKAQVNEGKRLMPGQDPDKTISDMFQND 554
QY 547 RNGDGKVTAEERKPL---XDOEAKHD 568
Db 555 RNQDGKITAEELKLGKSDQERVHE 579

RESULT 7
Q9H3N3 PRELIMINARY; PRT; 582 AA.
AC Q9H3N3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65kDa FK506-binding protein.
GN HFKBP65.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Mitsuomori C., Morikawa N., Isogai T., Ota T., Yuri K., Nishikawa T.,
RA Masuho Y., Nagahara K.;
RT "The human 65kDa FK506-binding protein (HFKBP65) gene induces the
RT morphological differentiation of NT2 neuron precursor cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045981; BAB20974.1; -.
DR HSSP; F20081; IYAT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 582 AA; 64305 MW; 04B25129A1D4D92 CRC64;

Query Match 57.1%; Score 1744; DB 4; Length 582;
Best Local Similarity 56.4%; Pred. No. 1.5e-130;
Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;

QY 10 PP-----PLILLILLVWT-----QAPAVAGLGSDAELQIERFVDPCEPTRVSGD 55
Db 6 PPSHSLRLPLQLLLLVQAVGRGLGRASPAGPLED--VVIERYHIPRACPREVQMGD 63
QY 56 FVRYHYVGTFFDQKPDSSYDRSTFNVFVGKGLITGMDOALVGMCVNERFVKIPKPL 115
Db 64 FVRYHYNGTFEDGKPDSSYDRNTLVAIVVGRLITGMDOALVGMCVNERRLIVPHL 123
QY 116 AYGNERNVSGVIPPNSVHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRHYNG 175
Db 124 GYGSIGLAGLIPPDATLYFDVLLDVNWKEDTVQVSTLLRPPHCPRMVQDGFVRHYNG 183

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Query Match 49.8%; Score 1522; DB 4; Length 481;  
 Best Local Similarity 57.5%; Pred. No. 5.8e-113;  
 Matches 276; Conservative 89; Mismatches 109; Indels 6; Gaps 4;

QY 94 MDQALVGMCMNRRFVKIPKPLAYGNERSVGVIPNSVLHFDVLLMDIWNSEDOVQIHTY 153  
 DB 1 MDRGLMGMCMNRRRLIIVPHLYGSGIGLACLPDPTLYFDVLLDVWNKEDTVQVSTL 60

QY 154 FKPPSPRTIQVSDFRVRYHYNGTFLDGTLPDSSHNRMKTYDTYVIGIWLIPGMDKGLLGM 213  
 DB 61 LRPHPCRMVQDGFVRVYHYNGTLLDGTSPDTSYSGKGYDTYVVGSLIKGMDQGLLGM 120

QY 214 CVYGEKRIITPPPLAYCEGDGDKIPQASLVDFDVALLDHNPDKSISIEKNKVPENCER 273  
 DB 121 CGERRKRIITPPPLAYGEKGYGVIPQASLVFHVLLIDVHNPKDAVQLETLELPQGCVR 180

QY 274 IQSGDFLTHYNGTLLDGTLPDSSYSNRNRTFDYIQQGVIPVGMDEGLLGVCIGEKRXI 333  
 DB 181 RAGAGDFMRYHYNGSLMDGTLPDSSYSNRNTHYNTYIQQGVIPGMDOQLQGACNGERRI 240

QY 334 VPPHLYGEGEGGN-IPGSALVDFDIHVDHNPDSISITSHYKPPD-CSVLSKKGDY 391  
 DB 241 TTPHLYAYGNGTGDGKIPGSALVDFHNPADVVEIRTLSPSETCNETTKLGD 300

QY 392 LKYHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDGLREMCVGEKRTVILPPLHG 451  
 DB 301 VRYHNCSLDGTQFTSHDYGAPQEBATLGANKVIEGLDTGLQGMCGERRQLIVPPLHA 360

QY 452 YBAGVDGVPGSALVDFDIEXELVAGLPEGYFIWNGEVSPLNLFREIDKDGNGEVILLE 511  
 DB 361 HGBSGARG-VPGSALLFEVELSVREDGLPTGYLFVWHKDPANLFDMDLNKDGVEPPE 419

QY 512 EFSEYIHAQVAGSGKGLAPGDAELIVKNMFTNDRNGDGKVTAEFFKL---XDQEAH 568  
 DB 420 EFSTFIKAQVSEKGRMLPQDPEKTIQDMFQNDQNGDKITVDELKLSDEDEERVHE 479

RESULT 10  
 Q9H6J3 PRELIMINARY; PRT; 355 AA.

ID Q9H6J3  
 AC Q9H6J3;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CDNA: FLJ22221 fis, clone HRC01651.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
 RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,  
 RA Nakamura Y., Isegai T., Sugano S.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK025874; BAB15266.1; -.  
 DR HSSP; Q00688; IPBK.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR InterPro; IPR001179; FKBP\_PPase.  
 DR Pfam; PF00036; ehand; 2.  
 DR Pfam; PF00254; FKBP; 2.  
 DR SMART; SM00054; EFh; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 1.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN 1.  
 DR PROSITE; PS50059; FKBP\_PPase\_3; 2.  
 DR PROSITE; PS50059; FKBP\_PPase\_3; 2.  
 SQ SEQUENCE 355 AA; 38950 MW; DBECAF4B8618BF54F CRC64;

Query Match 27.7%; Score 845.5; DB 4; Length 355;  
 Best Local Similarity 45.5%; Pred. No. 3.3e-59;  
 Matches 161; Conservative 58; Mismatches 68; Indels 67; Gaps 4;

QY 281 LTYHNGTLLDGTLPDSSYSNRNRTFDYIQQGVIPVGMDEGLLGVCIGEKRTVIVPPLHG 340  
 DB 1 MRHYNGSLMDGTLPDSSYSNRNTHYNTYIQQGVIPGMDOQLQGACNGERRITIPPLHA 60

QY 341 YBEGEGGN-IPGSALVDFDIHVDHNPDSISITSHYKPPD-CSVLSKKGDY 348  
 DB 61 YGNGTDSIGFLQGSAPLRPFSGBGQPSLGRGGYGTPEPAYPQDPAVLGASVSPVKW 120

QY 349 -----IPGSALVDFDIHVDHNPDSISITSHYKPPD-CSVLSKKGDY 397  
 DB 121 ASHADPQGDGKIPGSALVDFHNPADVVEIRTLSPSETCNETTKLGDVFRYHYN 180

QY 398 ASLLDGTLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDGLREMCVGEKRTVILPPLHG 457  
 DB 181 CSLDGTQFTSHDYGAPQEBATLGANKVIEGLDTGLQGMCGERRQLIVPPLHAGESGA 240

QY 458 DGEVPGSALVDFDIEXELVAGLPEGYFIWNGEVSPLNLFREIDKDGNGEVILLE 517  
 DB 241 RG-VPGSALLFEVELSVREDGLPTGYLFVWHKDPANLFDMDLNKDGVEPPEFTFI 299

QY 518 HAQVAGSGKGLAPGDAELIVKNMFTNDRNGDGKVTAEFFKL---XDQEAH 568  
 DB 300 KAQVSEKGRMLPQDPEKTIQDMFQNDQNGDKITVDELKLSDEDEERVHE 353

RESULT 11  
 Q9UF89 PRELIMINARY; PRT; 262 AA.

ID Q9UF89  
 AC Q9UF89;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 28.9 kDa protein (Fragment).  
 GN DKPZP58610821.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=UTERUS;  
 RA Outenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL131116; CAB61418.1; -.  
 DR HSSP; Q00688; IPBK.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR InterPro; IPR001179; FKBP\_PPase.  
 DR Pfam; PF00036; ehand; 2.  
 DR Pfam; PF00254; FKBP; 2.  
 DR SMART; SM00054; EFh; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 1.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN 1.  
 DR PROSITE; PS50059; FKBP\_PPase\_3; 2.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 262 AA; 28926 MW; A9630934276BA84E CRC64;

Query Match 24.1%; Score 736; DB 4; Length 262;  
 Best Local Similarity 52.5%; Pred. No. 1.1e-50;  
 Matches 137; Conservative 53; Mismatches 65; Indels 6; Gaps 4;

QY 313 YIIPGMDEGLLGVCIGEKRTVIVPPLHGVEEGGN-IPGSALVDFDIHVDHNPDSI 371  
 DB 1 YIIPGMDOQLQGACNGERRITIPPLHAYGNGTQDKIPGSALVDFHNPADV 60

QY 372 SITSHYKPPD-CSVLSKKGDYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMD 430  
 DB 61 EIRTLSPSETCNETTKLGDVFRYHYNCSLLDGTQFTSHDYGAPQEBATLGANKVIEGLD 120

QY 431 MGLREMCVGEKRTVILPPLHGVEAGVDGVPGSALVDFDIEXELVAGLPEGYFIWNG 490  
 DB 431 MGLREMCVGEKRTVILPPLHGVEAGVDGVPGSALVDFDIEXELVAGLPEGYFIWNG 490

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Db 121 TGLQCMCVGERRQLIVPPHLAGHSGARG-VPGSAVLFEVLVSREDGLPTGYLFWVHK 179
Qy 491 EVSNLFEEDKCGNGVLEEFSSYTHAQSAGKGLAPGDAELIVKMFNFTDNRNGD 550
Db 180 DPPANLFDMDLNKDGVPPEEFSTFIKAQVSEGRGLMPCQDFEKTIGDMFQNDNRQD 239
Qy 551 GKVTAEFFKL---XDQBAKHD 568
Db 240 GKITVDELKLSDEDEERVHE 260

RESULT 12
Q98UD7 PRELIMINARY; PRT; 137 AA.
AC Q98UD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FK506-binding protein (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Anano T., Yoshizato K.;
RT "Isolation of genes involved in intestinal remodeling during anuran
RT metamorphosis."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170336; AAK11511.1; -.
DR HSP; Q00688; 1PBK.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00454; FKBP_PPASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPASE_3; 1.
FT NON TER 1
FT NON TER 137
SQ SEQUENCE 137 AA; 15070 MW; DC3EGACABB24F625 CRC64;

Query Match 15.2%; Score 464.5; DB 13; Length 137;
Best Local Similarity 65.0%; Pred. No. 1.9e-29;
Matches 89; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

Qy 146 DQVQIHTYFKPPSPRTIQVSDFVRYHYNGTFLDGTLDSSSHRMKTYDVTYVGIGWLIIPG 205
Db 1 DEVQITTIHKASPCNRSQDSDFVRYHYNGTLDGTLYDSSYSRSTTYDVTYVGSGLIKG 60
Qy 206 MDKGLLGMVGEKRIITIPPLAYGEDGDKIPQASLIVFDVALLDLHNPKDSISIEK 265
Db 61 MDMLGLMGACGEKRIITIPPLAYGERGYTIIPQASLIVFHLIDFHPNPKDGTIVQNG 120
Qy 266 VVPENCERI-SQSGDFL 281
Db 121 VVPGVQTAKTGVYV 137

RESULT 13
O16309 PRELIMINARY; PRT; 261 AA.
AC O16309;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 29.1 kDa protein.
GN C05C8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;

Db 121 TGLQCMCVGERRQLIVPPHLAGHSGARG-VPGSAVLFEVLVSREDGLPTGYLFWVHK 179
Qy 491 EVSNLFEEDKCGNGVLEEFSSYTHAQSAGKGLAPGDAELIVKMFNFTDNRNGD 550
Db 180 DPPANLFDMDLNKDGVPPEEFSTFIKAQVSEGRGLMPCQDFEKTIGDMFQNDNRQD 239
Qy 551 GKVTAEFFKL---XDQBAKHD 568
Db 240 GKITVDELKLSDEDEERVHE 260

RESULT 14
P91180 PRELIMINARY; PRT; 264 AA.
ID P91180;
AC P91180;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 29.9 kDa protein.
GN C50F2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
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RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX Sammons L., Wohldmann P.;
RT "The sequence of C. elegans cosmid C05C8."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX Waterston R.;
RT "Direct Submission."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016430; AAB65370.1; -.
DR HSP; P27124; 1ROT.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00254; FKBP; 2.
DR PROSITE; PS00014; ER TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 261 AA; 29080 MW; 545A8B82B1BE26AD CRC64;

Query Match 11.3%; Score 344.5; DB 5; Length 261;
Best Local Similarity 32.2%; Pred. No. 1.9e-19;
Matches 73; Conservative 51; Mismatches 92; Indels 11; Gaps 4;

Qy 260 ISTENKVVPCNERISQSGDFLTVHYNGTLDGTLDSSYSRNRKTPDTYIGQGVIPGMD 319
Db 30 IEIKKIGDSKCKYKESGDLQGFYKLSKEGKVGISNFGQ-KPYFTYLGKEVHGME 88
Qy 320 EGLGVCGICGRXIVPPHLYGEGEGRNIPGSA-VLVFDIHVIDFHPN-----SDS 370
Db 89 IAMEGMCVGEQRKVIIPPEQGFDEG-DEVEGKETLYYFVELKSIIPRPKPAKWITDEG 147
Qy 371 ISTSHYKPPDCSVLKKGYLKVHYNASLLDGTLDSTWNLGKTYNVLGSGGVVLGMD 430
Db 148 VHIHTHEVGCTEKAQGTLLHQQTINLEDSFIDSSWRNRPPIFKMGSGGVIKGMD 207
Qy 431 MGLRMCVGEKRTVIIIPPHLYGEGAGVDGEVPGSAVLVDIEKLELV 477
Db 208 IAMEGMCVGEQRKVIIPPELAYENGRRPPIPGNSYLHFDLSLEKLV 254

RESULT 14
P91180 PRELIMINARY; PRT; 264 AA.
ID P91180;
AC P91180;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 29.9 kDa protein.
GN C50F2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
```

RA Du Z., Le T.T.;  
RT "The sequence of C. elegans cosmid C50F2.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U80445; AAB37799.1; -.  
DR HSSP; P20071; 1B4.  
DR InterPro; IPR000886; ER target.  
DR InterPro; IPR001179; FKBP\_PPIase.  
DR Pfam; PF00254; FKBP; 2.  
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; UNKNOWN 2.  
DR PROSITE; PS00059; FKBP\_PPIASE\_3; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 264 AA; 29937 MW; 90B79FD4F978A2D CRC64;  
  
Query Match 11.2%; Score 343; DB 5; Length 264;  
Best Local Similarity 37.5%; Pred. No. 2.5e-19;  
Matches 87; Conservative 36; Mismatches 93; Indels 16; Gaps 7;  
  
QY 142 WNSD--QVQIHTYFKPPSPRTIQVSDFVRYHYNGTFLDGTFLDSSHNRMKTYDYVGI 199  
DB 24 WKDEDGLEIKIIRPIKAECPIKSDQDGVLDQWYKLSKDKGKEIGSNFNK-KPYTFTLGK 82  
  
QY 200 GWLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKD-IPGQASLVFDVALLDLH---- 254  
DB 83 GQVIPGMRAMTGMCKGKRVIPGNLFGDKGRERDNKEDQTLTYTVQLVDLFRVAP 142  
  
QY 255 ----NPKDSISIE--NKVVPENCERISQSGDPLFYHYNGTLLDGTFLDSSYSNRNRTFDY 308  
DB 143 GEKWTDEGIVIEQTHKIDEDCKK-SKSGDTIHQQYVVLHLEDGTFLDSSFSRNAPFIK 201  
  
QY 309 IGQGVIPGMDGELGVCIGEKRIIVPPLHLYGEGRG-NIPGSALVFDI 359  
DB 202 LNNNEVIKMDIAMTGMCEGERRQVIPSDFGYGDDGRAPAIKGRARLYFDI 253

RESULT 15  
Q95Q60 PRELIMINARY; PRT; 300 AA.  
AC Q95Q60;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical 34.2 kDa protein.  
GN C50F2.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Du Z., Le T.T.;  
RT "The sequence of C. elegans cosmid C50F2.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U80445; AAK68259.1; -.  
DR InterPro; IPR000886; ER target.  
DR InterPro; IPR001179; FKBP\_PPIase.  
DR Pfam; PF00254; FKBP; 2.  
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; UNKNOWN 2.  
DR PROSITE; PS00059; FKBP\_PPIASE\_3; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 300 AA; 34160 MW; A70252F2736CF36C CRC64;  
  
Query Match 11.2%; Score 343; DB 5; Length 300;  
Best Local Similarity 37.5%; Pred. No. 3e-19;  
Matches 87; Conservative 36; Mismatches 93; Indels 16; Gaps 7;  
  
QY 142 WNSD--QVQIHTYFKPPSPRTIQVSDFVRYHYNGTFLDGTFLDSSHNRMKTYDYVGI 199  
DB 60 WKDEDGLEIKIIRPIKAECPIKSDQDGVLDQWYKLSKDKGKEIGSNFNK-KPYTFTLGK 118  
  
QY 200 GWLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKD-IPGQASLVFDVALLDLH---- 254  
DB 119 GQVIPGMRAMTGMCKGKRVIPGNLFGDKGRERDNKEDQTLTYTVQLVDLFRVAP 178  
  
QY 255 ----NPKDSISIE--NKVVPENCERISQSGDPLFYHYNGTLLDGTFLDSSYSNRNRTFDY 308  
DB 179 GEKWTDEGIVIEQTHKIDEDCKK-SKSGDTIHQQYVVLHLEDGTFLDSSFSRNAPFIK 237  
  
QY 309 IGQGVIPGMDGELGVCIGEKRIIVPPLHLYGEGRG-NIPGSALVFDI 359  
DB 238 LNNNEVIKMDIAMTGMCEGERRQVIPSDFGYGDDGRAPAIKGRARLYFDI 289

Search completed: April 26, 2003, 06:55:46  
Job time : 51.5014 secs



GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 27.2202 Seconds  
(without alignments)  
1899.367 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGETGWLIPGMDKGLGMC.....VNDFFPLKLLYFTNLNIFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002.\*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
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7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*  
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16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.\*  
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18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description                 |
|------------|--------|-------------|--------|----|-----------------------------|
| 1          | 2106   | 100.0       | 388    | 20 | AAY23887 Amino acid sequenc |
| 2          | 1616   | 76.7        | 570    | 22 | AAB88320 Human membrane or  |
| 3          | 1606   | 76.3        | 541    | 20 | AAY23886 Amino acid sequenc |
| 4          | 1000.5 | 47.5        | 434    | 21 | AAB54356 Human pancreatic c |
| 5          | 1000.5 | 47.5        | 582    | 21 | AAB12128 Hydrophobic domain |
| 6          | 1000.5 | 47.5        | 582    | 21 | AAY52294 Human isomerase ho |
| 7          | 1000.5 | 47.5        | 582    | 22 | AAG79226 Amino acid sequenc |
| 8          | 937.5  | 47.4        | 441    | 20 | RAY23885 Amino acid sequenc |
| 9          | 771.5  | 36.6        | 1241   | 22 | ABG05911 Novel human diagno |
| 10         | 618    | 29.3        | 127    | 22 | AAO5027 Human polypeptide   |

|    |       |      |     |    |                             |
|----|-------|------|-----|----|-----------------------------|
| 11 | 544.5 | 25.9 | 366 | 21 | AAB57114 Human prostate can |
| 12 | 541.5 | 25.7 | 316 | 20 | AAY23884 Amino acid sequenc |
| 13 | 484.5 | 23.0 | 166 | 23 | ABP41125 Human ovarian anti |
| 14 | 287   | 13.6 | 216 | 22 | ABB64697 Drosophila melanog |
| 15 | 275   | 13.1 | 138 | 22 | ABB69722 Drosophila melanog |
| 16 | 265.5 | 12.6 | 159 | 21 | AAG10995 Arabidopsis thalia |
| 17 | 265.5 | 12.6 | 163 | 21 | AAG10994 Arabidopsis thalia |
| 18 | 259   | 12.3 | 146 | 21 | AAG19838 Arabidopsis thalia |
| 19 | 259   | 12.3 | 152 | 21 | AAG39837 Arabidopsis thalia |
| 20 | 259   | 12.3 | 153 | 21 | AAG39836 Arabidopsis thalia |
| 21 | 253   | 12.0 | 146 | 21 | AAG05732 Arabidopsis thalia |
| 22 | 253   | 12.0 | 152 | 21 | AAG05731 Arabidopsis thalia |
| 23 | 253   | 12.0 | 153 | 21 | AAG05730 Arabidopsis thalia |
| 24 | 250.5 | 11.9 | 163 | 23 | ABG60082 Human DTHP polype  |
| 25 | 247.5 | 11.8 | 141 | 17 | AAG93551 Human FKBP-13 immu |
| 26 | 241.5 | 11.5 | 137 | 22 | AAB87656 Bovine mammary tis |
| 27 | 237.5 | 11.3 | 135 | 22 | AAG70716 S cerevisiae apopt |
| 28 | 236   | 11.2 | 143 | 13 | AAR28980 hrFKBP. Homo sapi  |
| 29 | 234.5 | 11.1 | 211 | 20 | AAY41706 Human PRO381 prote |
| 30 | 234.5 | 11.1 | 211 | 20 | AAY01458 Polypeptide fragme |
| 31 | 234.5 | 11.1 | 211 | 21 | AAB44262 Human PRO381 (UNO3 |
| 32 | 234.5 | 11.1 | 211 | 21 | AAB44021 Human PRO381 prote |
| 33 | 234.5 | 11.1 | 211 | 21 | AAB33463 Human PRO381 prote |
| 34 | 234.5 | 11.1 | 211 | 21 | AAY94975 Human secreted pro |
| 35 | 234.5 | 11.1 | 211 | 22 | AAU12363 Human PRO381 polyp |
| 36 | 234.5 | 11.1 | 211 | 21 | AAB50909 Human PRO381 prote |
| 37 | 234.5 | 11.1 | 211 | 22 | AAB50952 Human PRO381 prote |
| 38 | 231   | 11.0 | 241 | 22 | AAG75623 Human colon cancer |
| 39 | 230.5 | 10.9 | 239 | 21 | AAB43704 Secreted protein e |
| 40 | 227.5 | 10.8 | 212 | 20 | AA01401 Secreted protein e  |
| 41 | 225   | 10.7 | 219 | 20 | AAW88556 Human secreted p   |
| 42 | 225   | 10.7 | 219 | 22 | ABBS0323 Human PRO1304 prot |
| 43 | 225   | 10.7 | 222 | 21 | AAB24429 Amino acid sequenc |
| 44 | 225   | 10.7 | 222 | 21 | RAY84868 Human PRO1304 (UNQ |
| 45 | 225   | 10.7 | 222 | 21 | RAY99391                    |

#### ALIGNMENTS

##### RESULT 1

RAY23887

ID AAY23887 standard; Protein; 388 AA.

XX AAY23887;

DT 21-SEP-1999 (first entry)

DE Amino acid sequence of a FK506 binding protein 65.

XX Human; FK506 binding protein; FKBP65; immune system disorder;  
KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
KW blood coagulation disorder; blood platelet disorder; wound;  
KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
KW hypersensitivity; blood group incompatibility; organ rejection;  
KW graft versus host disease; inflammatory condition;  
KW ischemia-reperfusion injury; endotoxin lethality; arthritis;  
KW complement-mediated hyperacute rejection; nephritis; lung injury;  
KW inflammatory bowel disease; Crohn's disease; infection.

XX Homo sapiens.

XX WO9935160-A1.

XX 15-JUL-1999.

XX 06-JAN-1999; 99WO-US00120.

XX 09-JAN-1998; 98US-0070875.

XX (HUMA-) HUMAN GENOME SCI INC.

XX





Db 315 IFQMDGGLGVCIGEKRRIVVPHLGYGEGRGNIIPGSAVLVFDIHFVDFHNPDSISIT 374  
 QY 181 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 240  
 Db 375 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 434  
 QY 241 EMCVGEKRTVIIPPHLGYGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFVWNGEVSP 300  
 Db 435 EMCVGEKRTVIIPPHLGYGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFVWNGEVSP 494  
 QY 301 NLFEEINK 308  
 Db 495 NLFEEIDK 502

## RESULT 3

RAY23886  
 ID AAY23886 standard; Protein; 541 AA.

XX AC AAY23886;

XX DT 21-SEP-1999 (first entry)

XX DE Amino acid sequence of a FK506 binding protein.

XX Human; FK506 binding protein; FKBP65; immune system disorder;  
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
 KW blood coagulation disorder; blood platelet disorder; wound;  
 KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
 KW hypersensitivity; blood group incompatibility; organ rejection;  
 KW graft versus host disease; inflammatory condition;  
 KW ischemia-reperfusion injury; endotoxin lethality; arthritis;  
 KW complement-mediated hyperacute rejection; nephritis; lung injury;  
 KW inflammatory bowel disease; Crohn's disease; infection.

XX OS Homo sapiens.

XX PN WO9935160-A1.

XX PD 15-JUL-1999.

XX PF 06-JAN-1999; 99WO-US00120.

XX PR 09-JAN-1998; 98US-0070875.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Moore PA, Ruben SM, Wei Y;

XX DR WPI; 1999-430382/36.

XX DR N-PSDB; AAX86147.

XX PT New nucleic acids encoding human FK506 binding proteins

XX PS Claim 12; Fig 3; 87pp; English.

XX The present sequence represents human FK506 binding protein 65 (FKBP65).  
 CC The polypeptide or polynucleotide may be useful in treating deficiencies  
 CC or disorders of the immune system, by activating or inhibiting the  
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune  
 CC cells. They may be useful in treating or detecting deficiencies or  
 CC disorders of hematopoietic cells, to increase differentiation and  
 CC proliferation of hematopoietic cells including the pluripotent stem  
 CC cells, in an effort to treat those disorders associated with a decrease  
 CC in certain types of hematopoietic cells. They can be used to modulate  
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood  
 CC coagulation disorders, blood platelet disorders or wounds resulting from  
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
 CC strokes or scarring. They can also treat autoimmune disorders, allergic  
 CC reactions and conditions such as asthma (particularly allergic asthma) or  
 CC other respiratory problems, anaphylaxis, hypersensitivity to an antigenic

CC molecule, or blood group incompatibility, organ rejection or graft versus  
 CC host disease, inflammatory conditions, both chronic and acute, including  
 CC inflammation associated with infection, ischemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,  
 CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel  
 CC disease, or Crohn's disease. They can also be used to treat viral,  
 CC bacterial, fungal and parasitic infections.

XX SQ Sequence 541 AA;

Query Match 76.3%; Score 1606; DB 20; Length 541;  
 Best Local Similarity 98.1%; Pred. No. 2.8e-152;  
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TYGEIGWLIPGMDKGLGKLMVCVGEKRIITIPFLAYGEDGDKDIPGQASLVFVALLDLH 60  
 Db 195 TYVGIGWLIPGMDKGLGKLMVCVGEKRIITIPFLAYGEDGDKDIPGQASLVFVALLDLH 254  
 QY 61 NPKDSISIEKVVPCERISQSGDFLRVHYNGTLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 120  
 Db 255 NPKDSISIEKVVPCERISQSGDFLRVHYNGTLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 314  
 QY 121 IFQMDGGLGVCIGEKRRIVVPHLGYGEGRGNIIPGSAVLVFDIHFVDFHNPDSISIT 180  
 Db 315 IFQMDGGLGVCIGEKRRIVVPHLGYGEGRGNIIPGSAVLVFDIHFVDFHNPDSISIT 374  
 QY 181 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 240  
 Db 375 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 434  
 QY 241 EMCVGEKRTVIIPPHLGYGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFVWNGEVSP 300  
 Db 435 EMCVGEKRTVIIPPHLGYGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFVWNGEVSP 494  
 QY 301 NLFEEINK 308  
 Db 495 NLFEEIDK 502

## RESULT 4

AAB54356

ID AAB54356 standard; Protein; 434 AA.

XX AC AAB54356;

XX DT 09-MAR-2001 (first entry)

XX DE Human pancreatic cancer antigen protein sequence SEQ ID NO:808.

XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
 KW detection; diagnosis; identification; cytostatic; neuroprotective;  
 KW neoplastic; immunomodulatory; relaxant; contraceptive; gynecological;  
 KW antineoplastic; cardiac; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic;  
 KW neutral; immune system; muscular; reproductive; gastrointestinal;  
 KW pulmonary; cardiovascular; renal; proliferative.

XX OS Homo sapiens.

XX PN WO200055320-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05989.

XX PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2000-579444/54.

XX DR N-PSDB; AAC99121.

XX New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition -  
 XX  
 PS Claim 11; Page 1260-1261; 1379pp; English.  
 XX  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, nontropic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiac and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 XX Sequence 434 AA;

Query Match 47.5%; Score 1000.5; DB 21; Length 434;  
 Best Local Similarity 55.1%; Pred. No. 1.4e-91;  
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;  
 QY 1 TYGEIGWLPMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPQASLVFVALLDLH 60  
 DB 55 TVGSGWLIKQMDQGLGMCGERKRIITPPFLAYGEKGYGTVIPQASLVFVALLDVH 114  
 QY 61 NPKDSISIEKVPENCERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTFTYIGQYV 120  
 DB 115 NPKDAVQLETLPLPGCVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRFTFTYIGQYI 174  
 QY 121 IPGMDGGLGVCIKRRIVPPHLYGEGRGN-IPGSALVDFIDHFNPSDSISI 179  
 DB 175 IPGMDQGLQACMGERRITIPPHLAYGNGTGDKIIPGSALVDFIDHFNPDVVEI 234  
 QY 180 TSHYKPPD-CSVLSKKGDKYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLMGDMG 238  
 DB 235 RTLSRPFSETCNETTKLGDVFRHYNGSLDGTQLFTSHDYGAPQEAATLGANKVIEGLDTG 294  
 QY 239 IREMCVGEKRTVIIPPHLYGEGAGVDGVPGSALVDFIDHFNPSDSISI 298  
 DB 295 LQGMCGVRRQLIVPPHLAGHSGARG-VPGSAVLFFVELVSRDGLFTGYLFWHDKP 353  
 QY 299 SPNLFEE--EINK-----VTFCCPFVSWRRWYPEGKGL 330  
 DB 354 PANLFEDMDLNKDGVEPPEEFSTFI-----KAQVSEKGRLL 389

RESULT 5  
 AAB12128  
 ID AAB12128 standard; Protein; 582 AA.  
 XX  
 AC AAB12128;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE Hydrophobic domain protein from clone HP02991 isolated from KB cells.  
 XX  
 KW Human; secreted protein; membrane protein; hydrophobic domain;  
 KW proliferation control; differentiation induction; material transport;

KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;  
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;  
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;  
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200029448-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 17-NOV-1999; 99W0-JP06412.  
 XX  
 PR 17-NOV-1998; 98JP-0326255.  
 PR 22-DEC-1998; 98JP-0364315.  
 PR 16-MAR-1999; 99JP-0069811.  
 PR 27-APR-1999; 99JP-0119299.  
 PR 19-MAY-1999; 99JP-0138169.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 XX  
 PI Kato S, Kimura T;  
 XX  
 DR WPI; 2000-387753/33.  
 DR N-PSDB; AAG62001, AAG62011.  
 XX  
 XX Proteins comprising hydrophobic regions, such as secretory and membrane  
 PT proteins, useful in research and diagnostics and having various  
 PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,  
 PT haemostatic, thrombolytic -  
 XX  
 PS Claim 1; Page 230-232; 410pp; English.

Secretory proteins play important roles in the proliferation control, the  
 differentiation induction, the material transport and the biophylaxis of  
 cells. Membrane proteins have important roles as signal receptors, ion  
 channels and transporters. The present sequence is a human protein which  
 has at least one hydrophobic domain. This protein may be a secretory or a  
 membrane protein. The present protein may have cytokine and cell  
 proliferation/differentiation activity, immune stimulating or suppressing  
 activity, haematopoiesis activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, anti-inflammatory activity and tumour  
 CC inhibition activity. The present protein could therefore be used for  
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's  
 CC disease, and cancer.

XX Sequence 582 AA;

Query Match 47.5%; Score 1000.5; DB 21; Length 582;  
 Best Local Similarity 55.1%; Pred. No. 2.2e-91;  
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY 1 TYGEIGWLPMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPQASLVFVALLDLH 60  
 DB 203 TVGSGWLIKQMDQGLGMCGERKRIITPPFLAYGEKGYGTVIPQASLVFVALLDVH 262  
 QY 61 NPKDSISIEKVPENCERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTFTYIGQYV 120  
 DB 263 NPKDAVQLETLPLPGCVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRFTFTYIGQYI 322  
 QY 121 IPGMDGGLGVCIKRRIVPPHLYGEGRGN-IPGSALVDFIDHFNPSDSISI 179  
 DB 323 IPGMDQGLQACMGERRITIPPHLAYGNGTGDKIIPGSALVDFIDHFNPDVVEI 382  
 QY 180 TSHYKPPD-CSVLSKKGDKYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLMGDMG 238  
 DB 383 RTLSRPFSETCNETTKLGDVFRHYNGSLDGTQLFTSHDYGAPQEAATLGANKVIEGLDTG 442  
 QY 239 IREMCVGEKRTVIIPPHLYGEGAGVDGVPGSALVDFIDHFNPSDSISI 298  
 DB 443 LQGMCGVRRQLIVPPHLAGHSGARG-VPGSAVLFFVELVSRDGLFTGYLFWHDKP 501



```

Db      383  RTLSRPSETCNETTKLGDVRYHYNCSLLDGTQLFTSHDYGAPOEATLGANKVIEGLDTG 442
QY      239  LREMCVGEKRTVIIPPHLGYGEAGVDGVRGSAVLVDIELLELVAGLPEGYMFIWNGEV 298
Db      443  LQGMCVGERROLIVPPHLAGESGARG-VPGSAVLLFEVLVSREDGLTGYLFVFWHKDP 501
QY      299  SPNLFE--EINK-----VTFPCPFVSWRRWYPEGKQL 330
Db      502  PANLFEDMDLNKDGVEPPEEFSTFI-----KAQVSEKGRGL 537

RESULT 7
AAG79226
ID      AAG79226 standard; Protein; 582 AA.
XX
AC      AAG79226;
XX
DT      03-JAN-2002 (first entry)
XX
XX      Amino acid sequence of neurotrophic factor expression-inducing agent.
XX      Human; neurotrophic factor; PSEC56; nerve growth factor;
XX      neurite outgrowth; neural disease; dementia; cerebral embolism;
XX      spinal injury; peripheral nerve disease.
XX      Homo sapiens.
XX      WO200173024-A1.
XX      04-OCT-2001.
XX      30-MAR-2001; 2001WO-JP02768.
XX      31-MAR-2000; 2000JP-0101300.
XX      (HELI-) HELIX RES INST.
XX      (WELF-) WELFIDE CORP.
XX      Mitsumori C, Morikawa N, Hayaashi K, Nagahari K, Ota T, Hio Y;
XX      Nishikawa T, Isogai T, Kawasaki M, Hashimoto K, Kishimoto T;
XX      WPI; 2001-616501/71.
XX      N-PSDB; AA165835.

Neurotrophic factor expression-inducing agent, applicable in developing
drugs for neural diseases e.g. dementia, cerebral embolism, spinal
injury and peripheral nerve diseases by screening their regulatory
effect
XX
XX      Example 1; Page 34-38; 42pp; Japanese.
XX
XX      The present sequence represents a human neurotrophic factor
XX      expression-inducing agent. The polypeptide is designated PSEC56.
XX      The PSEC56 protein is used to increase nerve growth factor providing
XX      neurite outgrowth effect, which is applicable in developing drugs for
XX      neural diseases e.g. dementia, cerebral embolism, spinal injury and
XX      peripheral nerve diseases, with use of PSEC56 as the neurotrophic
XX      factor expression-inducing agent which can be applied in a system to
XX      study induction and secretion mechanism of neurotrophic factor.
XX
XX      Sequence 582 AA;
SQ
Query Match 47.5%; Score 1000.5; DB 22; Length 582;
Best Local Similarity 55.1%; Pred. NO. 2.2e-91;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY      1  TYGEIGWLIPGMDKGLGMCVEKRIITPPFLAYGEDGDGKDIPQASLVFEDVALLDLH 60
Db      203  TVVSGWLKNGDQGLGMCPEKRIITPPFLAYGEKGYGVIPQASLVFVHLLIDVH 262
QY      61  NPKDSISINVKVPENCERISQSGPLRVHYNGTLLDGTLPDSSYSRNHTFTYIGQYV 120

```

```

Db      263  NPKDAVOLETLPPGCVRRAGADPMRYHNGSLMDGTLFDSYSRNHTYNTYIGQYI 322
QY      121  IPGMDEGLLGVICGEKRIIVPPHLYGEGRGN-IPGSAVLVDIHDVDFHNPDSGISI 179
Db      323  IPGMDQGLQACWGERRIITPPHLYAGENGTDGKIPGSAVLIPNVHVIDFHPADVVEI 382
QY      180  TSHYKPPD-CSVLSKSGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238
Db      383  RTLSRPSETCNETTKLGDVRYHYNCSLLDGTQLFTSHDYGAPOEATLGANKVIEGLDTG 442
QY      239  LREMCVGEKRTVIIPPHLGYGEAGVDGVRGSAVLVDIELLELVAGLPEGYMFIWNGEV 298
Db      443  LQGMCVGERROLIVPPHLAGESGARG-VPGSAVLLFEVLVSREDGLTGYLFVFWHKDP 501
QY      299  SPNLFE--EINK-----VTFPCPFVSWRRWYPEGKQL 330
Db      502  PANLFEDMDLNKDGVEPPEEFSTFI-----KAQVSEKGRGL 537

RESULT 8
AAY23885
ID      AAY23885 standard; Protein; 441 AA.
XX
AC      AAY23885;
XX
DT      21-SEP-1999 (first entry)
XX
XX      Amino acid sequence of a FK506 binding protein 65.
XX      Human; FK506 binding protein; FKBP65; immune system disorder;
XX      immune cell; hematopoietic cell disorder; thrombolytic activity;
XX      blood coagulation disorder; blood platelet disorder; wound;
XX      heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
XX      asthma; allergic asthma; respiratory problem; anaphylaxis;
XX      hypersensitivity; blood group incompatibility; organ rejection;
XX      graft versus host disease; inflammatory condition;
XX      ischemia-reperfusion injury; endotoxin lethality; arthritis;
XX      complement-mediated hyperacute rejection; nephritis; lung injury;
XX      inflammatory bowel disease; Crohn's disease; infection.
XX      Homo sapiens.
XX      WO9935160-A1.
XX      15-JUL-1999.
XX      06-JAN-1999; 99WO-US00120.
XX      09-JAN-1998; 98US-0070875.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Moore PA, Ruben SM, Wei Y;
XX      WPI; 1999-430382/36.
XX      N-PSDB; AAX86146.

New nucleic acids encoding human FK506 binding proteins
XX
XX      Claim 12; Fig 2; 87pp; English.
XX
XX      The present sequence represents a human FK506 binding protein 65
XX      (FKBP65). It is a splice variant of the sequence given in AAX86145.
XX      The polypeptide or polynucleotide may be useful in treating deficiencies
XX      or disorders of the immune system, by activating or inhibiting the
XX      proliferation, differentiation, or mobilization (chemotaxis) of immune
XX      cells. They may be useful in treating or detecting deficiencies or
XX      disorders of hematopoietic cells, to increase differentiation and
XX      proliferation of hematopoietic cells including the pluripotent stem
XX      cells, in an effort to treat those disorders associated with a decrease
XX      in certain types of hematopoietic cells. They can be used to modulate
XX      hemostatic or thrombolytic activity, e.g. an increase can treat blood
XX      coagulation disorders, blood platelet disorders or wounds resulting from

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CC trauma, surgery or other causes, or a decrease can treat heart attacks,  
CC strokes or scarring. They can also treat autoimmune disorders, allergic  
CC reactions and conditions such as asthma (particularly allergic asthma)  
CC or other respiratory problems, anaphylaxis, hypersensitivity to an  
CC antigenic molecule, or blood group incompatibility, organ rejection or  
CC graft versus host disease, inflammatory conditions, both chronic and  
CC acute, including inflammation associated with infection,  
CC ischaemia-reperfusion injury, endotoxin lethality, arthritis,  
CC complement-mediated hyperacute rejection, nephritis, cytokine or  
CC chemokine-induced lung injury, inflammatory bowel disease, or Crohn's  
CC disease. They can also be used to treat viral, bacterial, fungal and  
CC parasitic infections.

XX SQ Sequence 441 AA;

Query Match 47.4%; Score 997.5; DB 20; Length 441;

Best Local Similarity 55.1%; Pred. No. 2.9e-91;

Matches 189; Conservative 59; Mismatches 74; Indels 21; Gaps 6;

Qy 1 TYGEIGWLPMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPGQASLVFDVALLDLH 60

Db 62 TYVSGWLLIKGMDQGLGMCVGEKRIITPPFLAYGEKGYGTIVPPQASLVFHVLLDVH 121

Qy 61 NPKDSISIEKVVPENCERISQSGDFLRYHNGTLLDGTLLFDSYSRNRFTDVIQGYV 120

Db 122 NPKDAVQLETLELPQCVRRAGDFMRHYNGSLMDGTLLFDSYSRNRFTDVIQGYI 181

Qy 121 IPQMDGGLGVCIGEKRRIVVPHLGYGEGRGN-IPGSALVFDIHDVDFHNPDSISI 179

Db 182 IPQMDGGLGACWGERRITIPHLAYGENTGDKIPGSALVIFNVHVDHNPADVVEI 241

Qy 180 TSHYKPPD-CVLSKKGDKYLYKHYNASLLDGTLLDSTWNIGKTYNIVLGSQVVLGMDG 238

Db 242 RTLSRPSSETCNETTKLGDVFRVHYNCSLDGTQLFTSHDYGAQOEATLGANKVIEGLDTG 301

Qy 239 LREMVCGERKTVIIPHLGYGEAGVGEVPGSALVFDIELLELVAGLPEGYMFVWGEV 298

Db 302 LQGMCGERKQLIVPPLHLAGESARG-VPGSALLFEVLVSREDGLTGYLFWHNDP 360

Qy 299 SPNLFEEI--NK-----VTFPCPFVSWRRWYPEGRLQ 330

Db 361 PANLFEDIDLKDGVEVPPEFSTFI-----KAQVSEKGR 396

RESULT 9

ABG05911

ID ABG05911 standard; Protein; 1241 AA.

XX AC ABG05911;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #5902.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PX Drmanac RT, Liu C, Tang YT;

XX XX WPI; 2001-639362/73.

DR N-PSDB; AAS70098.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX

PS Claim 20; SEQ ID No 36270; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1241 AA;

Query Match 36.6%; Score 771.5; DB 22; Length 1241;

Best Local Similarity 49.2%; Pred. No. 7.1e-68;

Matches 146; Conservative 48; Mismatches 62; Indels 41; Gaps 4;

Qy 7 WLII-PGMDKGLGMCVGEKRIITPPFLAYGEDGDKD----- 43

Db 6 WLADQGHGPGAAGHVSWEKEIIIPFLAYGEKGYEGGKGKGFRRGKNQASTVSCS 65

Qy 44 -----IPQASLVFDVALLDLHNPKDSISIEKVVPENCERISQSGDFL 87

Db 66 GCILHEGIQPTQTGTIVPPQASLVFHVLLIDVHNPDAVQLETLELPQCVRRAGADFM 125

Qy 88 RYHNGTLLDGTLLFDSYSRNRFTDVIQGYVIFGMDGGLGVCIGEKRRIVVPHLGY 147

Db 126 RYHYNGSLMDGTLLFDSYSRNRHTYNTYIGGYIIPGMDGGLGVCIGEKRRITIPPLAY 185

Qy 148 GEEGRGN-IPGSALVFDIHDVDFHNPDSISITSHYKPPD-CVLSKKGDKYLYKHYNAS 205

Db 186 GENGTDKIPGSALVIFNVHVDHNPADVBEIRTLRPSSETCNETTKLGDVFRVHYNCS 245

Qy 206 LLDGTLLDSTWNIGKTYNIVLGSQVVLGMDGMLREMCVGEKRTVIIPHLGYGEAG 262

Db 246 LLDGTQLFTSHDYGAQOEATLGANKVIEGLDTLQGMCGERKQLIVPPLHLAGESG 302

RESULT 10

AAO05027

ID AAO05027 standard; Protein; 127 AA.

XX AC AAO05027;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 18919.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.

XX XX

OS Homo sapiens.  
 PN WO200164835-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US04927.  
 XX  
 PR 28-FEB-2000; 2000US-0515126.  
 PR 18-MAY-2000; 2000US-0577409.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-514838/56.  
 DR N-PSDB; AAI84958.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX  
 PS Claim 20; SEQ ID NO 18919; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AAI79941-AAI93941) and  
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 127 AA;  
 Query Match 29.3%; Score 618; DB 22; Length 127;  
 Best Local Similarity 97.5%; Pred. No. 6e-54;  
 Matches 117; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 189 SVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNVLGSGQVVLGMDGLREMCVGER 248  
 DB 2 SVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNVLGSGQVVLGMDGLREMCVGER 61  
 QY 249 TVIIPPHLYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFVWNGEVSFNLFEINK 308  
 DB 62 TVIIPPHLYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFVWNGEVSFNLFEIDK 121  
 RESULT 11  
 AAB57114  
 ID AAB57114 standard; Protein; 366 AA.  
 XX  
 AC AAB57114;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1692.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587513/55.  
 DR N-PSDB; AAF16317.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer -  
 XX  
 PS Claim 11; Page 2162-2164; 2338pp; English.  
 XX  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 366 AA;  
 Query Match 25.9%; Score 544.5; DB 21; Length 366;  
 Best Local Similarity 48.5%; Pred. No. 7.2e-46;  
 Matches 98; Conservative 37; Mismatches 66; Indels 1; Gaps 1;  
 QY 62 PKDSISIEKVVPCNERISQSGDFLRHYNGTLLDGTLLDFTDSSYSRNRFTDTYIQGGYVI 121  
 DB 76 FLEDVIERHYHPRACPREVQMGDFVRYHYNGTTFEDGKGFSSYDRNTLVAIVGVGRLL 135  
 QY 122 PQMDEGLLCVIGEKRRIVVPVPHLYGEGE-RGNIPGSAVLVFDIHDVDFNPSDSISIT 180  
 DB 136 TQMDRGLMGMCNRRRLIVPPHLYGSGISGLAGLIPPDATLYFDVLLDVWVKEDTVQVS 195  
 QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNVLGSGQVVLGMDGLR 240  
 DB 196 TLLRPPHPCPRVQMGDFVRYHYNGTLLDSTFDSYSKGGTYDYVGSGLIKGNDQGLL 255  
 QY 241 EMCVGERKTVIIPPHLYGEGAG 262  
 DB 256 GMPGERKRIIPPPFLAYGEG 277  
 RESULT 12  
 AAY23884  
 ID AAY23884 standard; Protein; 316 AA.  
 XX  
 AC AAY23884;  
 XX  
 DT 21-SEP-1999 (first entry)  
 XX  
 DE Amino acid sequence of FK506 binding protein 65 (FKBP65).  
 XX  
 KW Human; FK506 binding protein; FKBP65; immune system disorder;  
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;  
 KW blood coagulation disorder; blood platelet disorder; wound;

KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;  
KW asthma; allergic asthma; respiratory problem; anaphylaxis;  
KW hypersensitivity; blood group incompatibility; organ rejection;  
KW graft versus host disease; inflammatory condition;  
KW ischemia-reperfusion injury; endotoxin lethality; arthritis;  
KW complement-mediated hyperacute rejection; nephritis; lung injury;  
KW inflammatory bowel disease; Crohn's disease; infection.

XX Homo sapiens.

XX WO9935160-A1.

XX 15-JUL-1999.

XX 06-JAN-1999; 99WO-US00120.

XX 09-JAN-1998; 98US-0070875.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Wei Y;

XX WPI; 1999-430382/36.

XX N-PSDB; AAX86145.

XX New nucleic acids encoding human FK506 binding proteins

XX Claim 12; Fig 1; 87pp; English.

XX The present sequence represents human FK506 binding protein 65 (FKBP65).  
XX The polypeptide or polynucleotide may be useful in treating deficiencies  
XX or disorders of the immune system, by activating or inhibiting the  
XX proliferation, differentiation, or mobilization (chemotaxis) of immune  
XX cells. They may be useful in treating or detecting deficiencies or  
XX disorders of hematopoietic cells, to increase differentiation and  
XX proliferation of hematopoietic cells including the pluripotent stem  
XX cells, in an effort to treat those disorders associated with a decrease  
XX in certain types of hematopoietic cells. They can be used to modulate  
XX hemostatic or thrombolytic activity, e.g. an increase can treat blood  
XX coagulation disorders, blood platelet disorders or wounds resulting from  
XX trauma, surgery or other causes, or a decrease can treat heart attacks,  
XX strokes or scarring. They can also treat autoimmune disorders, allergic  
XX reactions and conditions such as asthma (particularly allergic asthma) or  
XX other respiratory problems, anaphylaxis, hypersensitivity to an antigenic  
XX molecule, or blood group incompatibility, organ rejection or graft versus  
XX host disease, inflammatory conditions, both chronic and acute, including  
XX inflammation associated with infection, ischemia-reperfusion injury,  
XX endotoxin lethality, arthritis, complement-mediated hyperacute rejection,  
XX nephritis, cytokine or chemokine induced lung injury, inflammatory bowel  
XX disease, or Crohn's disease. They can also be used to treat viral,  
XX bacterial, fungal and parasitic infections.

XX Sequence 316 AA;

Query Match 25.7%; Score 541.5; DB 20; Length 316;  
Best Local Similarity 48.0%; Pred. No. 1.2e-45;  
Matches 97; Conservative 38; Mismatches 66; Indels 1; Gaps 1;

QY 62 PKDSISIEKVVNCEKISGDFPLRYHYNGTLDGTLFSSYSRNRFTDYIGQYVI 121

Db 40 PLEDWIERHYIPRACPREVQMGDFVRYHYNGTFEDGKKFSSYDRNTLVAIVWGRLI 99

QY 122 PGMDEGLVCIGERRVTPPHLGYGEG-RGNTPGSNVLFVDHVDHFNPSISIT 180

Db 100 TGMDRGLMGCMVNRRLVPPHLYGSGIAGLIPPDATLFPDVLVLLDWNKEDTVQVS 159

QY 181 SHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLGMDMLR 240

Db 160 TLLRPPHCPRVQDGFVRYHYNGTLLDGTSPDTSYSGKGYDVTYVGSCLIKGMDQGLL 219

QY 241 EMCVGKRTVLIIPPHLYGGEAG 262

Db 220 GMPGQRKIIIPPLAYGEK 241

RESULT 13

ABP41125

ID ABP41125 standard; Protein; 166 AA.

XX ABP41125;

XX 23-AUG-2002 (first entry)

XX Human ovarian antigen HOFMO23, SEQ ID NO:2257.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
XX ovarian cancer; breast cancer; reproductive system disorder;  
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
XX inflammatory condition; immune disorder; blood disorder;  
XX cardiovascular disorder; respiratory disorder; neurological disorder;  
XX gastrointestinal disorder; urinary system disorder; drug screening;  
XX gene therapy; chromosome mapping; forensic analysis;  
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
XX antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ54202.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
XX useful in the prevention, treatment and diagnosis of cancer (e.g.  
XX ovarian cancer), immune disorders, cardiovascular disorders and  
XX neurological diseases -

XX Claim 11; SEQ ID No 2257; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
XX to the sequences of the invention. The invention additionally relates to  
XX recombinant vectors and host cells comprising human ovarian antigen  
XX polynucleotides, antibodies against human ovarian antigens, and the use  
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
XX treating, prognosing or preventing various ovary and/or breast-related  
XX disorders. Such conditions include ovarian cancer and breast cancer, and  
XX metastatic tumours of ovarian or breast origin, reproductive system  
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,  
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
XX vaginitis), immune disorders (e.g., congenital and acquired  
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,  
XX respiratory disorders, neurological disorders, gastrointestinal disorders  
XX and urinary system disorders. Ovarian antigen polypeptides and  
XX polynucleotides may also be used in screening for compounds which  
XX modulate ovarian antigen expression or activity. The polynucleotides may  
XX further be used for gene therapy, chromosome mapping, in the  
XX identification of individuals and in forensic analysis, and the  
XX polypeptides may be used as food additives or to prepare antibodies  
XX useful in disease diagnosis, drug targeting and phenotyping. The present  
XX sequence represents a human ovarian antigen of the invention.



CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 166 AA;

Query Match 23.0%; Score 484.5; DB 23; Length 166;  
 Best Local Similarity 54.9%; Pred. No. 2.3e-40;  
 Matches 89; Conservative 27; Mismatches 45; Indels 1; Gaps 1;  
 QY 25 RIITIPPELAYGEGDKDIPQASLVDFVALLDHNPKDSISIEKNKVPENCERISQSG 84  
 DB 4 RUVKIPPKLAYGEGVGVPDPDSVLFHFDVLLWNSDQVQVHTYFTPPSCRTIOXV 63  
 QY 85 DELRYHNGTLTDLGTLFDSYSNRRTDTYIGGVIPGMDGLLGVICGKRRIVVPPH 144  
 DB 64 DFVRHYNGTFLDGLTFLDSHNMKTYDTYIGVGLIPGMDKGLGVCGRKIITIPPF 123  
 QY 145 LQYGEGRG-NIPGSALVDFDIHVDHNPDSISITSHYKP 185  
 DB 124 LAYGEGDKDIPQASLVDFVALLDHNPKDSISIEKNKVP 165

# RESULT 14

AB664697  
 ID ABB64697 standard; Protein; 216 AA.

XX AC ABB64697;  
 XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 20883.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.  
 XX PR 23-MAR-2000; 2000US-191637P.  
 XX PA 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.  
 XX FI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL08800.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX interactions -  
 XX PS Disclosure; SEQ ID NO 20883; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX useful in developmental biology and in elucidating cell signalling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
 XX sequences (ABL01840-ABL16175) and the encoded proteins  
 XX (ABBS7737-ABBS72072).

XX CC The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from WIPO  
 XX at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 216 AA;

Query Match 13.6%; Score 287; DB 22; Length 216;  
 Best Local Similarity 37.4%; Pred. No. 2.4e-20;  
 Matches 65; Conservative 31; Mismatches 54; Indels 24; Gaps 5;

QY 47 QASLVDFVALLDHNPKDSISIEKNKV-----PENCERISQSGDPLRYHNGT 94  
 DB 3 KSNLVISCLLL-----VAISNLVRAQDLKVEIVISTPEVCEQSKNGSLTMHTGT 54  
 QY 95 L-LDGLTLPDSSYSNRRTDTYIGGVIPGMDGLLGVICGKRRIVVPPHGYGEGRG 153  
 DB 55 LQDKKPFDSFDRDQPTFQAGQVIGWQGLLANCMVGEKRRKTIIPQGLGDDQAG 114  
 QY 154 N-IPGSALVDFDIHVDHNPDSISITSHYKPPDCSVLSK--GDYLYHYNA 204  
 DB 115 NVIPPKATLFDVELINIGNAPPTTNVFKIEDDNADKQLSRESEVSEYLLKQMTA 168

# RESULT 15

ABB69722  
 ID ABB69722 standard; Protein; 138 AA.

XX AC ABB69722;  
 XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 35958.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.  
 XX PR 23-MAR-2000; 2000US-191637P.  
 XX PA 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.  
 XX FI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL13825.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX interactions -  
 XX PS Disclosure; SEQ ID NO 35958; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX useful in developmental biology and in elucidating cell signalling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX sequences (ABL01840-ABL16175) and the encoded proteins  
 XX (ABBS7737-ABBS72072).

XX CC The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from WIPO  
 XX at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 138 AA;

Query Match 13.1%; Score 275; DB 22; Length 138;  
 Best Local Similarity 46.4%; Pred. No. 2e-19;  
 Matches 58; Conservative 17; Mismatches 46; Indels 4; Gaps 2;



Qy 54 VALLDLHNPKDSISIENKVPENCERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTDT 113  
Db 13 VAASAASDPKVIGIKRV--ENCTRKAGGDLVHVYRGALQDGTDFDSSYSRGTPFSF 70  
Qy 114 YIQGYVIEGMEGLIGVCI GEKRRIVVPHLGYGEGR--GNIPGSVAVLVEDIHVIDFH 171  
Db 71 TLGARQVIKWDQGHILGMCGEQORKTIPPELGYGASGAGGKIPPNVAVLVEDTELKIE 130  
Qy 172 NPSDS 176  
Db 131 PRSGS 135

Search completed: April 26, 2003, 06:53:07  
Job time : 29.2202 secs



GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 9.81714 Seconds  
(without alignments)  
1162.874 Million cell updates/sec

Title: US-09-225-502-8  
Perfect score: 2106  
Sequence: 1 TYGETGWLIPGMDKGLGMC.....VNDPPLKLLYFTNLNIFVLM 388

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match % | Length | ID | Description      |
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| 1          | 1022   | 48.5          | 581    | 2  | US-08-989-386-7  |
| 2          | 1000.5 | 47.5          | 582    | 2  | US-08-989-386-1  |
| 3          | 247.5  | 11.8          | 141    | 1  | US-07-822-966B-6 |
| 4          | 247.5  | 11.8          | 142    | 1  | US-08-336-618-18 |
| 5          | 247.5  | 11.8          | 142    | 5  | PCT-US92-03993-7 |
| 6          | 237.5  | 11.3          | 135    | 1  | US-08-336-618-20 |
| 7          | 236.5  | 11.2          | 141    | 2  | US-08-803-899-6  |
| 8          | 235    | 11.2          | 104    | 3  | US-08-894-173-86 |
| 9          | 235    | 11.2          | 104    | 4  | US-09-398-193-86 |
| 10         | 232.5  | 11.0          | 105    | 3  | US-08-894-173-84 |
| 11         | 232.5  | 11.0          | 105    | 4  | US-09-398-193-84 |
| 12         | 218    | 10.4          | 99     | 5  | PCT-US92-03993-5 |
| 13         | 208.5  | 9.9           | 107    | 3  | US-08-894-173-69 |
| 14         | 208.5  | 9.9           | 107    | 3  | US-08-894-173-83 |
| 15         | 208.5  | 9.9           | 107    | 4  | US-09-398-193-69 |
| 16         | 208.5  | 9.9           | 107    | 4  | US-09-398-193-83 |
| 17         | 208.5  | 9.9           | 119    | 5  | PCT-US92-03993-1 |
| 18         | 208.5  | 9.9           | 120    | 1  | US-08-336-618-17 |
| 19         | 192    | 9.1           | 384    | 1  | US-08-707-793A-5 |
| 20         | 192    | 9.1           | 384    | 1  | US-08-707-792A-5 |
| 21         | 189    | 9.0           | 458    | 1  | US-08-336-618-24 |
| 22         | 188    | 8.9           | 113    | 5  | PCT-US92-03993-4 |
| 23         | 188    | 8.9           | 114    | 1  | US-08-336-618-16 |
| 24         | 188    | 8.9           | 459    | 1  | US-08-336-618-12 |
| 25         | 188    | 8.9           | 459    | 1  | US-08-336-618-26 |
| 26         | 186    | 8.8           | 107    | 3  | US-08-894-173-66 |
| 27         | 186    | 8.8           | 107    | 3  | US-08-894-173-79 |

Sequence 66, Appl  
Sequence 79, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 15, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 13, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 67, Appl  
Sequence 80, Appl  
Sequence 67, Appl

ALIGNMENTS

RESULT 1  
US-08-989-386-7  
; Sequence 7, Application US/08989386  
; Patent No. 5989860  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,386  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0443 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 581 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 894162  
US-08-989-386-7

Query Match 48.5%; Score 1022; DB 2; Length 581;  
Best Local Similarity 55.8%; Pred. No. 3,8e-100; Indels 20; Gaps 6;  
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;  
US-08-989-386-1

Qy 1 TYGIGWILIPGMDKGLGCMVCEKRIITIPPLAYGEDGDKIPGQASLVFDVALLDLH 60  
Db 202 TYVGSGLIKGMDQGLGCMCEKRIITIPPLAYGEKGYGVIPGQASLVFVLLDVH 261  
Qy 61 NPKDSISIKVVPNCERISQSGDFLRVHYNGTLLDGLTLPDSSYSRNRTPDTYIGQYV 120  
Db 262 NPKDVQLETLLEPGCVRRAGADFWRYHNGSLMDGLTFDSSYSRNRHTYVIGQYI 321  
Qy 121 IPGMDGGLGVICIGEKRIIVPPHLYGEBGRGN-IPGSVAVLFDIHDVDFHNPDSISI 179  
Db 322 IPGMDQGLQACIGERRITIPPLAYGENGTDGKIPGSVAVLFDVHVIDFHPNPDVEI 381  
Qy 180 TSHVKPPD-CSVLKSGDYLYKHYNASLLDGLTLLDSTWNLGKTYNIVLGSQGVVLGMDG 238  
Db 382 KTLSPENCNETSKIGDFIRHYHNCSLDGLTFLFSSHDYEAQBITLGANKVIEGLDRG 441  
Qy 239 LREMCVGEKRTVITIPPLHLYGEGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFIWNGEV 298  
Db 442 LQCMCVGERQLIVPPHLAHGARG-VPGSAVLLFEVLVSREDGLPTGYLVFYQDP 500  
Qy 239 SPNLFEEIN-----KVTFFCCPVSVWRWYPRGQGL-PODSNDSPPADL 342  
Db 501 STSLFEDMDLNGKEVPPPEEFSSFIKAQVN-----EGKRLMPGQDPDKTISDM 549

RESULT 2  
US-08-989-386-1  
; Sequence 1, Application US/08989386  
; Patent No. 5989860  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-SEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,386  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0443 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 582 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: OVARUT01  
; CLONE: 2255114  
; US-08-989-386-1

Query Match 47.5%; Score 1000.5; DB 2; Length 582;  
Best Local Similarity 55.1%; Pred. No. 7.5e-98;  
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;  
US-08-989-386-1

Qy 1 TYGIGWILIPGMDKGLGCMVCEKRIITIPPLAYGEDGDKIPGQASLVFDVALLDLH 60  
Db 203 TYVGSGLIKGMDQGLGCMCEKRIITIPPLAYGEKGYGVIPGQASLVFVLLDVH 262  
Qy 61 NPKDSISIKVVPNCERISQSGDFLRVHYNGTLLDGLTLPDSSYSRNRTPDTYIGQYV 120  
Db 263 NPKDVQLETLLEPGCVRRAGADFWRYHNGSLMDGLTFDSSYSRNRHTYVIGQYI 322  
Qy 121 IPGMDGGLGVICIGEKRIIVPPHLYGEBGRGN-IPGSVAVLFDIHDVDFHNPDSISI 179  
Db 323 IPGMDQGLQACIGERRITIPPLAYGENGTDGKIPGSVAVLFDVHVIDFHPNPDVEI 382  
Qy 180 TSHVKPPD-CSVLKSGDYLYKHYNASLLDGLTLLDSTWNLGKTYNIVLGSQGVVLGMDG 238  
Db 383 RLSRPETCNETKIGDFVRYHNCSLDGLTFLFSSHDYEAQBITLGANKVIEGLDTG 442  
Qy 239 LREMCVGEKRTVITIPPLHLYGEGAGVDGVPGSVAVLFDIELLELVAGLPEGYMFIWNGEV 298  
Db 443 LQCMCVGERQLIVPPHLAHGARG-VPGSAVLLFEVLVSREDGLPTGYLVFYWPKDP 501  
Qy 299 SPNLFEEIN-----KVTFFCCPVSVWRWYPRGQGL 330  
Db 502 PANLFEDMDLNGKEVPPPEEFSTFI-----KAQVSEKGRGL 537

RESULT 3  
US-07-822-966B-6  
; Sequence 6, Application US/07822966B  
; Patent No. 5498597  
; GENERAL INFORMATION:  
; APPLICANT: Steven J. Burakoff  
; APPLICANT: Stuart L. Schreiber  
; APPLICANT: Barbara E. Blier  
; TITLE OF INVENTION: PKBP-13, AN FK506-BINDING  
; TITLE OF INVENTION: IMMUNOPHILIN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/822,966B  
; FILING DATE: January 17, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frazer, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/052001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid



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; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,618
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VPI91-06A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-618-20

Query Match 11.3%; Score 237.5; DB 1; Length 135;
Best Local Similarity 43.1%; Pred. No. 1.6e-17;
Matches 53; Conservative 22; Mismatches 41; Indels 7; Gaps 3;

QY 49 SLVFDVALLDHPKDSISIEKVVPENCERISQSGDFLRHYNGTLLD-GTLFDSYSR 107
DB 13 STILAGLSLDL-----EIGIKRIPVEDCLIKAMPDGVKRVHYTGSLLESGTVFDSYSR 67

QY 108 NRTDITYGQYVPGMDGLGVCIGEKRRIVVPHLGYGEEG-RGNIPGSALVDFDIH 166
DB 68 GSPIAPLEGVGRVIKWDQGVAGNVCVCKKQLQIPSSLAYGERGVPGVIPPADLVFDE 127

QY 167 VID 169
DB 128 LVD 130

RESULT 7
US-08-803-899-6
; Sequence 6, Application US/08803899
; Patent No. 5912224
; GENERAL INFORMATION:
; APPLICANT: DONAHOE, PATRICIA K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; CELLULAR RESPONSE TO TGF-BETA LIGANDS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON

; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,899
; FILING DATE: 02/21/1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/012,054
; FILING DATE: 02/22/1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4240001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-803-899-6

Query Match 11.2%; Score 236.5; DB 2; Length 141;
Best Local Similarity 46.7%; Pred. No. 2.2e-17;
Matches 50; Conservative 18; Mismatches 36; Indels 3; Gaps 2;

QY 63 KDSISIEKVVPENCERISQSGDFLRHYNGTLLDGTLLFDSYSRNRFTDVIYGGYVIP 122
DB 29 KLIQGVKRV--DHCPIKSRKGDVLMHYTKLEDGTEFDSLSLPQNPQFVSLGTGVK 86

QY 123 GMDGLGVCIGEKRRIVVPHLGYGEEG-RNIPGSALVDFDIHVI 168
DB 87 GWDQGLGVCIGEKRRIVVPHLGYGEEG-RNIPGSALVDFDIHVI 168

RESULT 8
US-08-894-173-86
; Sequence 86, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 86
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Yeast
; US-08-894-173-86

Query Match 11.2%; Score 235; DB 3; Length 104;
Best Local Similarity 47.9%; Pred. No. 2e-17;
Matches 46; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 187 DCSVLKKGDKYLYKHYNASLLDGTLLDSTWNLGTYNTIVLGSQGVVLGMDGLREMCVGE 246
DB 8 DCLIKAMPDGVKRVHYTGSLLESGTVFDSYSRGSPIAFELGVRVKGWDQGVAGNVCVGE 67

QY 247 KETVLIIPHLGYGEEGVDGVPGSALVDFDIHLEL 282
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Db 68 KRKLQIPSSLAYGERGVGVIPPSADLVDFVELVDV 103
RESULT 9
US-09-398-193-86
; Sequence 86, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Yeast
US-09-398-193-86
Query Match 11.2%; Score 235; DB 4; Length 104;
Best Local Similarity 47.9%; Pred. No. 2e-17;
Matches 46; Conservative 16; Mismatches 34; Indels 0; Gaps 0;
QY 187 DCSVLSKKGDYLVKHYNASLIDGTLDTWNLGKTYNIVLGSQGVVLGMDGLREMCVGE 246
DB 8 DCLIKAMPDGKKVHYTGSLESTGTFDSSYSRGSPIAFELGVRGVIRKGDQGVAGMCVGE 67
QY 247 KRTVLIIPHLGYGAGVDGVPGSVAVLVDIELLEL 282
DB 68 KRKLQIPSSLAYGERGVGVIPPSADLVDFVELVDV 103
RESULT 10
US-08-894-173-84
; Sequence 84, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
US-08-894-173-84
Query Match 11.0%; Score 232.5; DB 3; Length 105;
Best Local Similarity 49.5%; Pred. No. 3.7e-17;
Matches 47; Conservative 15; Mismatches 32; Indels 1; Gaps 1;
QY 75 ENCRISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTDYIGQYVIPGMDGELGVCIG 134
DB 3 DHCPIKSRKGDVLMHMYTKLEDGTFDSSLPQNPQPFVSLGTGQVIKGDQGLGMYEG 62
QY 135 EKRRIVVPPHLGYGEGR-GNIPGSVAVLVDIHI 168
DB 63 EKRRKLVIPSELGYGERGAPPKIPGGATLVFEVELL 97
RESULT 11
US-09-398-193-84
; Sequence 84, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
US-09-398-193-84
Query Match 11.0%; Score 232.5; DB 4; Length 105;
Best Local Similarity 49.5%; Pred. No. 3.7e-17;
Matches 47; Conservative 15; Mismatches 32; Indels 1; Gaps 1;
QY 75 ENCRISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTDYIGQYVIPGMDGELGVCIG 134
DB 3 DHCPIKSRKGDVLMHMYTKLEDGTFDSSLPQNPQPFVSLGTGQVIKGDQGLGMYEG 62
QY 135 EKRRIVVPPHLGYGEGR-GNIPGSVAVLVDIHI 168
DB 63 EKRRKLVIPSELGYGERGAPPKIPGGATLVFEVELL 97
PCT-US92-03993-5
; Sequence 5, Application PC/TUS9203993
; GENERAL INFORMATION:
; APPLICANT: Harding, Matthew W.
; TITLE OF INVENTION: RPKBP: A NOVEL PROLYL ISOMERASE AND
; TITLE OF INVENTION: RAPAMYCIN/PK506 BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03993
; FILING DATE: 19920507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/697,113
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VPI91-05A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-03993-5
Query Match 10.4%; Score 218; DB 5; Length 99;
Best Local Similarity 49.4%; Pred. No. 1.2e-15;
Matches 44; Conservative 14; Mismatches 29; Indels 2; Gaps 1;
QY 63 KDSISIENKVVPCNERISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTDYIGQYVIP 122
DB 8 KLQIGVKRV--DHCPIKSRKGDVLMHMYTKLEDGTFDSSLPQNPQPFVSLGTGQVIK 65
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```

; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-09-398-193-69

Query Match          9.9%; Score 208.5; DB 4; Length
Best Local Similarity 44.0%; Pred. No. 1.4e-14;
Matches 40; Conservative 16; Mismatches -34; Indels

Qy      79  RISQSGDLRLRYHNYGTLTDGTLFDSSYSGRNRFDFYIGGVYIPGNDGDE
Db      14  RETRGRDNDVHYKGLVTSKKFKFDASYORGEPLNTFVGQGVQVTKGWDGE

Qy      139  IVPVPHLGYGEEGRGN-IPGSAYLVFDIHVI 168
          : : : : : : : : : : : : : : : : : : : :
          : : : : : : : : : : : : : : : : : : : :
Db      74  LTIAPHLAYGNRAVGGIIPANSTLIFEELV 104

Search completed: April 26, 2003, 06:49:53
Job time : 12.0671 secs

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GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2003, 06:51:02 ; Search time 12.2714 Seconds  
(without alignments)  
2533.559 Million cell updates/sec

Title: US-09-225-502-8  
Perfect score: 2106  
Sequence: 1 TYGEIGWLIPGMDKGLLGMC.....VNDFFPLKLLYFTTNLNFVLM 388

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB\_PEP.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB\_PEP.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB\_PEP.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2106   | 100.0       | 388    | 10 | US-09-225-502-8    |
| 2          | 1606   | 76.3        | 574    | 10 | US-09-225-502-6    |
| 3          | 1000.5 | 47.5        | 434    | 10 | US-09-925-297-808  |
| 4          | 997.5  | 47.4        | 441    | 10 | US-09-225-502-4    |
| 5          | 544.5  | 25.9        | 366    | 10 | US-09-925-300-1692 |
| 6          | 541.5  | 25.7        | 336    | 10 | US-09-225-502-2    |
| 7          | 234.5  | 11.1        | 211    | 9  | US-09-978-295A-145 |
| 8          | 234.5  | 11.1        | 211    | 9  | US-09-978-697-145  |
| 9          | 234.5  | 11.1        | 211    | 9  | US-09-978-192A-145 |
| 10         | 234.5  | 11.1        | 211    | 9  | US-09-999-832A-145 |
| 11         | 234.5  | 11.1        | 211    | 9  | US-10-001-054-4    |
| 12         | 234.5  | 11.1        | 211    | 9  | US-09-978-189-145  |
| 13         | 234.5  | 11.1        | 211    | 9  | US-10-028-072-384  |
| 14         | 234.5  | 11.1        | 211    | 9  | US-10-121-049-384  |
| 15         | 234.5  | 11.1        | 211    | 9  | US-10-123-904-384  |
| 16         | 234.5  | 11.1        | 211    | 9  | US-10-140-470-384  |
| 17         | 234.5  | 11.1        | 211    | 9  | US-10-175-746-384  |
| 18         | 234.5  | 11.1        | 211    | 9  | US-10-176-918-384  |
| 19         | 234.5  | 11.1        | 211    | 9  | US-10-176-921-384  |

|    |       |      |     |   |                    |                   |
|----|-------|------|-----|---|--------------------|-------------------|
| 20 | 234.5 | 11.1 | 211 | 9 | US-10-137-865-384  | Sequence 384, App |
| 21 | 234.5 | 11.1 | 211 | 9 | US-10-140-474-384  | Sequence 384, App |
| 22 | 234.5 | 11.1 | 211 | 9 | US-10-142-431-384  | Sequence 384, App |
| 23 | 234.5 | 11.1 | 211 | 9 | US-10-143-114-384  | Sequence 384, App |
| 24 | 234.5 | 11.1 | 211 | 9 | US-10-140-002-384  | Sequence 384, App |
| 25 | 234.5 | 11.1 | 211 | 9 | US-09-978-608A-145 | Sequence 145, App |
| 26 | 234.5 | 11.1 | 211 | 9 | US-10-142-419-384  | Sequence 384, App |
| 27 | 234.5 | 11.1 | 211 | 9 | US-09-776-724A-189 | Sequence 189, App |
| 28 | 234.5 | 11.1 | 211 | 9 | US-09-978-131A-145 | Sequence 145, App |
| 29 | 234.5 | 11.1 | 211 | 9 | US-09-978-403A-145 | Sequence 145, App |
| 30 | 234.5 | 11.1 | 211 | 9 | US-09-978-604A-145 | Sequence 145, App |
| 31 | 234.5 | 11.1 | 211 | 9 | US-09-978-585A-145 | Sequence 145, App |
| 32 | 234.5 | 11.1 | 211 | 9 | US-10-017-081A-145 | Sequence 145, App |
| 33 | 234.5 | 11.1 | 211 | 9 | US-10-123-262-384  | Sequence 384, App |
| 34 | 234.5 | 11.1 | 211 | 9 | US-10-142-423-384  | Sequence 384, App |
| 35 | 234.5 | 11.1 | 211 | 9 | US-09-978-824-145  | Sequence 145, App |
| 36 | 234.5 | 11.1 | 211 | 9 | US-09-981-915A-145 | Sequence 145, App |
| 37 | 234.5 | 11.1 | 211 | 9 | US-09-999-833A-145 | Sequence 145, App |
| 38 | 234.5 | 11.1 | 211 | 9 | US-10-121-050-384  | Sequence 384, App |
| 39 | 234.5 | 11.1 | 211 | 9 | US-10-141-755-384  | Sequence 145, App |
| 40 | 234.5 | 11.1 | 211 | 9 | US-10-167-749-145  | Sequence 145, App |
| 41 | 234.5 | 11.1 | 211 | 9 | US-09-918-585A-145 | Sequence 384, App |
| 42 | 234.5 | 11.1 | 211 | 9 | US-10-143-032-384  | Sequence 145, App |
| 43 | 234.5 | 11.1 | 211 | 9 | US-09-978-423A-145 | Sequence 145, App |
| 44 | 234.5 | 11.1 | 211 | 9 | US-10-013-921A-145 | Sequence 145, App |
| 45 | 234.5 | 11.1 | 211 | 9 | US-10-123-108-384  | Sequence 384, App |

ALIGNMENTS

RESULT 1  
US-09-225-502-8  
; Sequence 8, Application US/09225502A  
; Patent No. US20020137127A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore et al.  
; TITLE OF INVENTION: Human FK506 Binding Proteins  
; FILE REFERENCE: PF392  
; CURRENT APPLICATION NUMBER: US/09/225,502A  
; CURRENT FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/070,875  
; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-225-502-8

Query Match 100.0%; Score 2106; DB 10; Length 388;  
Best Local Similarity 100.0%; Pred. No. 1.4e-188;  
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | TYGEIGWLIPGMDKGLIGMCVGEKRIITIPFLAYGEDGDKIPGQASLVFDVALLDLH    | 60  |
| DB | 1   | TYGEIGWLIPGMDKGLIGMCVGEKRIITIPFLAYGEDGDKIPGQASLVFDVALLDLH    | 60  |
| QY | 61  | NPKDSISIEKNVVPENCERISQSGDFLRYHYNGTLLDGLTLPDSSYSRNRFTDTYIGQYV | 120 |
| DB | 61  | NPKDSISIEKNVVPENCERISQSGDFLRYHYNGTLLDGLTLPDSSYSRNRFTDTYIGQYV | 120 |
| QY | 121 | IPGMDGLGVCIGEKRIIVVPHLGYGEGRGNI PGSAVLVFDHVIDFHNPSDSISIT     | 180 |
| DB | 121 | IPGMDGLGVCIGEKRIIVVPHLGYGEGRGNI PGSAVLVFDHVIDFHNPSDSISIT     | 180 |
| QY | 181 | SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTWNLKGTNYIVLGSQVVLGMDMGLR   | 240 |
| DB | 181 | SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTWNLKGTNYIVLGSQVVLGMDMGLR   | 240 |
| QY | 241 | EMCVGEKRIIVPHLGYGEGVDPGSAVLVFDIELLELVAGLPGYMFVWNGEYSP        | 300 |
| DB | 241 | EMCVGEKRIIVPHLGYGEGVDPGSAVLVFDIELLELVAGLPGYMFVWNGEYSP        | 300 |

Db 241 EMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFIWNGEVS 300  
 Qy 301 NLFBEINKVTFPCPFVSWRWYBEGRGQLQDSNDSPADLIPASWNNHMTATYPLFPN 360  
 Db 301 NLFBEINKVTFPCPFVSWRWYBEGRGQLQDSNDSPADLIPASWNNHMTATYPLFPN 360  
 Qy 361 GGGTYPEVNDPPLKLLYFTNLNFVLM 388  
 Db 361 GGGTYPEVNDPPLKLLYFTNLNFVLM 388

## RESULT 2

US-09-225-502-6  
 ; Sequence 6, Application US/09225502A  
 ; Patent No. US20020137127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Moore et al.  
 ; TITLE OF INVENTION: Human FK506 Binding Proteins  
 ; FILE REFERENCE: PF392  
 ; CURRENT APPLICATION NUMBER: US/09/225,502A  
 ; CURRENT FILING DATE: 1999-01-06  
 ; PRIOR FILING DATE: 1999-01-06  
 ; PRIOR FILING DATE: 1998-01-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 574  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-225-502-6

Query Match 76.3%; Score 1606; DB 10; Length 574;  
 Best Local Similarity 98.1%; Pred. No. 1.2e-141;  
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60  
 Db 195 TVVGIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 254  
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 120  
 Db 255 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 314  
 Qy 121 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 180  
 Db 315 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 374  
 Qy 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240  
 Db 375 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 434  
 Qy 241 EMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFIWNGEVS 300  
 Db 435 EMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFIWNGEVS 494  
 Qy 301 NLFBEINK 308  
 Db 495 NLFBEIDK 502

## RESULT 3

US-09-925-297-808  
 ; Sequence 808, Application US/09925297  
 ; Patent No. US20020081659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA105  
 ; CURRENT APPLICATION NUMBER: US/09/925,297  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 928  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 808  
 ; LENGTH: 434  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-925-297-808

Query Match 47.5%; Score 1000.5; DB 10; Length 434;  
 Best Local Similarity 55.1%; Pred. No. 3e-85;  
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60  
 Db 55 TVVGIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 114  
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 120  
 Db 115 NPKDAVQLELLEPPGCVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 174  
 Qy 121 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 179  
 Db 175 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 234  
 Qy 180 TSHYKPPD-CVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238  
 Db 235 RLSRPPSETCNETTKLGDVRYHYNCSSLDTQLFTSHDYGAQPEATIGANKVIEGLDTG 294  
 Qy 239 LREMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298  
 Db 295 LQMCVGERQLIVPPHLAGESGARG-VFGSAVLFEVELVSRDGLPTCYLFWHNDP 353  
 Qy 299 SPNLFEE--EINK-----VTFPCPFVSWRWYBEGRGQL 330  
 Db 354 PANLFEDMDLNKDGVEPPPEFTEFI-----KAQVSEKGRGL 389

## RESULT 4

US-09-225-502-4  
 ; Sequence 4, Application US/09225502A  
 ; Patent No. US20020137127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Moore et al.  
 ; TITLE OF INVENTION: Human FK506 Binding Proteins  
 ; FILE REFERENCE: PF392  
 ; CURRENT APPLICATION NUMBER: US/09/225,502A  
 ; CURRENT FILING DATE: 1999-01-06  
 ; PRIOR FILING DATE: 1999-01-06  
 ; PRIOR FILING DATE: 1998-01-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 441  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-225-502-4

Query Match 47.4%; Score 997.5; DB 10; Length 441;  
 Best Local Similarity 55.1%; Pred. No. 5.9e-85;  
 Matches 189; Conservative 59; Mismatches 74; Indels 21; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60  
 Db 62 TVVGIGWLIPGMDKGLGCMVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 121  
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 120  
 Db 122 NPKDAVQLELLEPPGCVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 181  
 Qy 121 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 179  
 Db 182 IPGMDGGLGVICIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIHDVDFHNPDSISIT 241

QY 180 TSHYKPPD-CSVLSKGGDYLYKHYNASLLDGTLLDSTWNLTKTYNIVLGSQVVLGMDMG 238  
DB 242 RTLSRPSFTCTNFTKGLDFVRYHYNGSLDGTQLFTSHDYGAQOBATLGANKVIEGLDTG 301  
QY 239 LREMCVGEKRTVIIPHLGVEAGVDCVEPGSAVLVDFDIELLELVAAGLPEGYMFIWNGEV 298  
DB 302 LQMCVGERQLIVPPHLAHGSGARG-VFGSAVLLEVEVLVSREDGLPTGYLFWHWDK 360  
QY 299 SPNLFBEI--NK-----VTFPCPFVSWRRWYPEGKQL 330  
DB 361 PANLFEDIDLKDGVEPPEFSTFI-----KAQVSEKGRGL 396

## RESULT 5

US-09-925-300-1692  
; Sequence 1692, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1692  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (8)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1692

Query Match 25.9%; Score 544.5; DB 10; Length 366;  
Best Local Similarity 48.5%; Pred. No. 9.5e-43;  
Matches 98; Conservative 37; Mismatches 66; Indels 1; Gaps 1;  
QY 62 PKDSISIEKVVPCNERISQSGDFLRHYNGTLLDGTFLFSSYSRNRFTFYIGQGYVI 121  
DB 76 PLEDVIERHYHIPRACPREVQMGDFVRYHYNGTFEDGKKFDSYDRNTLVAVIIVGVGRLLI 135  
QY 122 PGMDEGLLGVICIGKRRIVVPHLGYGEG-RGNIPGSAVLVDFDTHVIDFHNPSDSISIT 180  
DB 136 TGMDRGLMGCMVNERRLIVPHLGYGIGLAGLIPDPATLYFDVVLVDVWKNKEDTVQVS 195  
QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLTKTYNIVLGSQVVLGMDMGLR 240  
DB 196 TLLRPPHCPRMVQDGFVRYHYNGTLLDGTSPDTSYSGKGTDTYVVGSGWLKMGMDQGLL 255  
QY 241 EMCVGEKRTVIIPHLGVEAG 262  
DB 256 GMCPCGRRKIIIPPLAYGEGK 277

## RESULT 6

US-09-225-502-2  
; Sequence 2, Application US/09225502A  
; Patent No. US20020137127A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore et al.  
; TITLE OF INVENTION: Human FK506 Binding Proteins  
; FILE REFERENCE: PF392  
; CURRENT APPLICATION NUMBER: US/09/225,502A  
; CURRENT FILING DATE: 1999-01-06  
; PRIOR APPLICATION NUMBER: 60/070,875  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 09/918585  
; CURRENT FILING DATE: 2001-10-15  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; FILE REFERENCE: P2630PIC11  
; TITLE OF INVENTION: Acids Encoding the Same  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; CURRENT APPLICATION NUMBER: 2001-10-15  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03

; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-225-502-2

Query Match 25.7%; Score 541.5; DB 10; Length 336;  
Best Local Similarity 48.0%; Pred. No. 1.6e-42;  
Matches 97; Conservative 38; Mismatches 66; Indels 1; Gaps 1;  
QY 62 PKDSISIEKVVPCNERISQSGDFLRHYNGTLLDGTFLFSSYSRNRFTFYIGQGYVI 121  
DB 40 PLEDVIERHYHIPRACPREVQMGDFVRYHYNGTFEDGKKFDSYDRNTLVAVIIVGVGRLLI 99  
QY 122 PGMDEGLLGVICIGKRRIVVPHLGYGEG-RGNIPGSAVLVDFDTHVIDFHNPSDSISIT 180  
DB 100 TGMDRGLMGCMVNERRLIVPHLGYGIGLAGLIPDPATLYFDVVLVDVWKNKEDTVQVS 159  
QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLTKTYNIVLGSQVVLGMDMGLR 240  
DB 160 TLLRPPHCPRMVQDGFVRYHYNGTLLDGTSPDTSYSGKGTDTYVVGSGWLKMGMDQGLL 219  
QY 241 EMCVGEKRTVIIPHLGVEAG 262  
DB 220 GMCPCGRRKIIIPPLAYGEGK 241

## RESULT 7

US-09-978-295A-145  
; Sequence 145, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03

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| 1  | 1  | PRIOR FILING DATE: 1998-04-15       |  |
| 2  | 2  | PRIOR APPLICATION NUMBER: 60/081819 |  |
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| 46 | 46 | PRIOR APPLICATION NUMBER: 60/084366 |  |
| 47 | 47 | PRIOR FILING DATE: 1998-05-05       |  |
| 48 | 48 | PRIOR APPLICATION NUMBER: 60/084414 |  |
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| 56 | 56 | PRIOR APPLICATION NUMBER: 60/084640 |  |
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| 73 | 73 | PRIOR FILING DATE: 1998-05-15       |  |

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; PRIOR FILING DATE: 1998-04-15

Query Match      11.1%; Score 234.5; DB 9; Length 211;
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Db 72 GQPIWFTLGILEALKGWDQGLKGMVGEKRXLIIPALGYGKGGKIPPESTLIFNIDL 131
QY 168 IDFNH 172
Db 132 LEIRN 136

RESULT 8
US-09-978-697-145
; Sequence 145, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.1%; Score 234.5; DB 9; Length 211;  
Best Local Similarity 36.8%; Pred. No. 46-14; Indels 3; Gaps 2;

Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

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Db 132 LEIRN 136

## RESULT 9

US-09-978-192A-145  
; Sequence 145, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.1%; Score 234.5; DB 9; Length 211;  
Best Local Similarity 36.8%; Pred. No. 4e-14;  
Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

QY 51 VFDVALLDHNPKDSISIEKVVPCERISOSGDFLRHYNGTL-LDGTFLDSSYSRNR 109  
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QY 110 TFDYIGQGV--IPGMBGLGVCIGKGRIVVPHLYGEGGNIPGSAVLVFDIHV 167  
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QY 168 IDFN 172  
Db 132 LEIRN 136

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; Sequence 145, Application US/0999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
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US-10-001-054-4

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Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

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Db 12 LFTVSLICALPEPEPVKEVLQKPICHRTKTKGGDLMLVHYGYLGKQSLFHSHTKHNN 71

QY 110 TFDYVIGGVV--IPGMDEGLGVCIGEKRRIVPPHLYGGBEGRGNIPGSVAVLVFDIHV 167
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QY 168 IDFNH 172
Db 132 LEIRN 136

RESULT 12
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; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 2001-07-30
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Best Local Similarity 36.8%; Pred. No. 4e-14;  
Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

QY 51 VFDVALLDHNPKDSISIKNVKVPENCERISQSGDFLRYHYNGTL-LDGTLPDSSYSRNR 109  
Db 12 LFTVSLIGALIPPEVKIEVLQKPFICHRKTGGDLMLVHYEGYLEKDGSLFHSHTKHNN 71  
QY 110 TFDYIGQGVV--IPGMDEGLLGVICGKRRIVVPHLGYGEGRGNIQGSALVLPDIHV 167  
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Db 132 LEIRN 136

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; Publication No. US20030004311A1  
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; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17

|    |                                     |  |
|----|-------------------------------------|--|
| 1  | PRIOR FILING DATE: 1998-02-09       |  |
| 2  | PRIOR APPLICATION NUMBER: 60/077791 |  |
| 3  | PRIOR FILING DATE: 1998-03-12       |  |
| 4  | PRIOR APPLICATION NUMBER: 60/078910 |  |
| 5  | PRIOR FILING DATE: 1998-03-20       |  |
| 6  | PRIOR APPLICATION NUMBER: 60/079294 |  |
| 7  | PRIOR FILING DATE: 1998-03-25       |  |
| 8  | PRIOR APPLICATION NUMBER: 60/079663 |  |
| 9  | PRIOR FILING DATE: 1998-02-27       |  |
| 10 | PRIOR APPLICATION NUMBER: 60/079728 |  |
| 11 | PRIOR FILING DATE: 1998-03-27       |  |
| 12 | PRIOR APPLICATION NUMBER: 60/080165 |  |
| 13 | PRIOR FILING DATE: 1998-03-31       |  |
| 14 | PRIOR APPLICATION NUMBER: 60/081203 |  |
| 15 | PRIOR FILING DATE: 1998-04-09       |  |
| 16 | PRIOR APPLICATION NUMBER: 60/081229 |  |
| 17 | PRIOR FILING DATE: 1998-04-09       |  |
| 18 | PRIOR APPLICATION NUMBER: 60/081695 |  |
| 19 | PRIOR FILING DATE: 1998-04-14       |  |
| 20 | PRIOR APPLICATION NUMBER: 60/081817 |  |
| 21 | PRIOR FILING DATE: 1998-04-15       |  |
| 22 | PRIOR APPLICATION NUMBER: 60/081818 |  |
| 23 | PRIOR FILING DATE: 1998-04-15       |  |
| 24 | PRIOR APPLICATION NUMBER: 60/082999 |  |
| 25 | PRIOR FILING DATE: 1998-04-24       |  |
| 26 | PRIOR APPLICATION NUMBER: 60/083322 |  |
| 27 | PRIOR FILING DATE: 1998-04-28       |  |
| 28 | PRIOR APPLICATION NUMBER: 60/083545 |  |
| 29 | PRIOR FILING DATE: 1998-04-29       |  |
| 30 | PRIOR APPLICATION NUMBER: 60/084600 |  |
| 31 | PRIOR FILING DATE: 1998-05-07       |  |
| 32 | PRIOR APPLICATION NUMBER: 60/084627 |  |
| 33 | PRIOR FILING DATE: 1998-05-07       |  |
| 34 | PRIOR APPLICATION NUMBER: 60/084637 |  |
| 35 | PRIOR FILING DATE: 1998-05-07       |  |
| 36 | PRIOR APPLICATION NUMBER: 60/085149 |  |
| 37 | PRIOR FILING DATE: 1998-05-12       |  |
| 38 | PRIOR APPLICATION NUMBER: 60/085323 |  |
| 39 | PRIOR FILING DATE: 1998-05-13       |  |
| 40 | PRIOR APPLICATION NUMBER: 60/085338 |  |
| 41 | PRIOR FILING DATE: 1998-05-13       |  |
| 42 | PRIOR APPLICATION NUMBER: 60/085339 |  |
| 43 | PRIOR FILING DATE: 1998-05-13       |  |
| 44 | PRIOR APPLICATION NUMBER: 60/085579 |  |
| 45 | PRIOR FILING DATE: 1998-05-15       |  |
| 46 | PRIOR APPLICATION NUMBER: 60/085697 |  |
| 47 | PRIOR FILING DATE: 1998-05-15       |  |
| 48 | PRIOR APPLICATION NUMBER: 60/085704 |  |
| 49 | PRIOR FILING DATE: 1998-05-15       |  |
| 50 | PRIOR APPLICATION NUMBER: 60/086414 |  |
| 51 | PRIOR FILING DATE: 1998-05-22       |  |
| 52 | PRIOR APPLICATION NUMBER: 60/086430 |  |
| 53 | PRIOR FILING DATE: 1998-05-22       |  |
| 54 | PRIOR APPLICATION NUMBER: 60/087106 |  |
| 55 | PRIOR FILING DATE: 1998-05-28       |  |
| 56 | PRIOR APPLICATION NUMBER: 60/088026 |  |
| 57 | PRIOR FILING DATE: 1998-06-04       |  |
| 58 | PRIOR APPLICATION NUMBER: 60/088730 |  |
| 59 | PRIOR FILING DATE: 1998-06-10       |  |
| 60 | PRIOR APPLICATION NUMBER: 60/088741 |  |
| 61 | PRIOR FILING DATE: 1998-06-10       |  |
| 62 | PRIOR APPLICATION NUMBER: 60/088810 |  |
| 63 | PRIOR FILING DATE: 1998-06-17       |  |
| 64 | PRIOR APPLICATION NUMBER: 60/089599 |  |
| 65 | PRIOR FILING DATE: 1998-06-17       |  |
| 66 | PRIOR APPLICATION NUMBER: 60/089907 |  |
| 67 | PRIOR FILING DATE: 1998-06-18       |  |
| 68 | PRIOR APPLICATION NUMBER: 60/089947 |  |
| 69 | PRIOR FILING DATE: 1998-06-19       |  |



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 12.2714 Seconds  
(without alignments)  
3039.596 Million cell updates/sec

Title: US-09-225-502-8  
Perfect score: 2106  
Sequence: 1 TYGEIGWLIPGMQKGLGMC.....VNDFPLKLLYFTNLNYPVLM 388

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:\*  
1: Piri:\*  
2: Piri2:\*  
3: Piri3:\*  
4: Piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 1022  | 48.5        | 581    | 2 149669  | FKBP65 binding pro |
| 2          | 572.5 | 27.2        | 262    | 2 T42709  | hypothetical prote |
| 3          | 353.5 | 16.8        | 261    | 2 T31741  | hypothetical prote |
| 4          | 344   | 16.3        | 264    | 2 T29780  | hypothetical prote |
| 5          | 301.5 | 14.3        | 259    | 2 T27586  | hypothetical prote |
| 6          | 286.5 | 13.6        | 139    | 2 T21882  | hypothetical prote |
| 7          | 283.5 | 13.5        | 559    | 1 S55383  | peptidylprolyl iso |
| 8          | 273.5 | 13.0        | 241    | 2 E89251  | protein ZC455.10   |
| 9          | 269.5 | 12.8        | 311    | 1 S46228  | peptidylprolyl iso |
| 10         | 265.5 | 12.6        | 151    | 2 T12090  | probable peptidylp |
| 11         | 262   | 12.4        | 304    | 2 T761238 | probable peptidylp |
| 12         | 259   | 12.3        | 146    | 1 S71237  | hypothetical prote |
| 13         | 256.5 | 12.2        | 134    | 1 J70748  | probable peptidylp |
| 14         | 251.5 | 11.9        | 551    | 1 S72485  | FK506-binding prot |
| 15         | 251   | 11.9        | 140    | 2 I49668  | binding protein -  |
| 16         | 250.5 | 11.9        | 568    | 2 T06489  | probable peptidylp |
| 17         | 247.5 | 11.8        | 142    | 2 JCL365  | FK506/rapamycin-bi |
| 18         | 237.5 | 11.3        | 135    | 2 S25337  | peptidylprolyl iso |
| 19         | 214.5 | 10.2        | 113    | 2 A83180  | probable peptidylp |
| 20         | 211.5 | 10.0        | 165    | 2 A81878  | FKBP-type peptidyl |
| 21         | 208.5 | 9.9         | 120    | 2 S11090  | FK506-binding prot |
| 22         | 207.5 | 9.9         | 152    | 2 B75347  | peptidyl-prolyl ci |
| 23         | 198.5 | 9.4         | 201    | 1 S75144  | FKBP-type peptidyl |
| 24         | 198   | 9.4         | 290    | 2 T26537  | hypothetical prote |
| 25         | 196   | 9.3         | 157    | 2 C82431  | peptidyl-prolyl ci |
| 26         | 194   | 9.2         | 457    | 2 JC5422  | FK506-binding prot |
| 27         | 191   | 9.1         | 259    | 2 D82331  | peptidyl-prolyl ci |
| 28         | 189   | 9.0         | 458    | 1 A42386  | hsp 90-binding pro |

|    |       |     |     |          |                     |
|----|-------|-----|-----|----------|---------------------|
| 30 | 188   | 8.9 | 114 | 2 A33146 | peptidylprolyl iso  |
| 31 | 188   | 8.9 | 459 | 2 A46372 | immunophilin FKBP5  |
| 32 | 184.5 | 8.8 | 108 | 2 S54139 | FK506-binding prote |
| 33 | 183   | 8.7 | 431 | 2 T21594 | hypothetical prote  |
| 34 | 182   | 8.6 | 112 | 2 T40724 | peptidyl-prolyl ci  |
| 35 | 179   | 8.5 | 206 | 2 AE0429 | peptidylprolyl iso  |
| 36 | 178   | 8.5 | 108 | 2 T26539 | hypothetical prote  |
| 37 | 177   | 8.4 | 107 | 2 A61431 | peptidylprolyl iso  |
| 38 | 176   | 8.4 | 241 | 2 A64155 | hypothetical prote  |
| 39 | 175   | 8.3 | 205 | 2 F83075 | peptidyl-prolyl ci  |
| 40 | 175   | 8.3 | 458 | 2 JN0873 | immunophilin p59 -  |
| 41 | 174.5 | 8.3 | 105 | 2 A40211 | FK506-inhibitable   |
| 42 | 173   | 8.2 | 108 | 2 A35780 | peptidylprolyl iso  |
| 43 | 173   | 8.2 | 108 | 2 A42657 | FK506-binding prot  |
| 44 | 171.5 | 8.1 | 109 | 2 E82022 | peptidylprolyl iso  |
| 45 | 171.5 | 8.1 | 270 | 2 F91153 | FKBP-type peptidyl  |

ALIGNMENTS

RESULT 1

I49669  
FKBP65 binding protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I49669  
R:Simsek, S.L.; Kozak, C.A.; Winterstein, D.; Hegamyer, G.; Colburn, N.H.  
Genomics 18, 407-409, 1993  
A:Title: Sequence and localization of a novel FK506-binding protein to mouse chromosomes  
A:Reference number: A48920; MUID:94117013; PMID:7507077  
A:Accession: I49669  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-581 <RES>  
A:Cross-references: GB:L07063; NID:G894161; PIDN:AAC37678.1; PID:G894162  
F:61-108/Domain: BKBP-type peptidylprolyl isomerase homology  
F:173-220/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>  
F:285-332/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>  
F:398-445/Domain: BKBP-type peptidylprolyl isomerase homology <PPI4>

Query Match 48.5%; Score 1022; DB 2; Length 581;

Best Local Similarity 55.8%; Pred. No. 2.5e-76;

Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | TYGEIGWLIPGMQKGLGMCVGEKRIITIPFLAYGSDGDKDIPGQASLVDFVALLDLH  | 60  |
| DB | 202 | TVIGSGWLIKGMQGLGMCVGEKRIITIPFLAYGSDGDKDIPGQASLVDFVALLDLH   | 261 |
| QY | 61  | NPKDSISIKVVPENCERISQSGDFLRHYNGTLLDGTLDSSYSRNPFTDVIQGYV     | 120 |
| DB | 262 | NPKDTVQLETLFPOGCVRAVAGDFMRHYNGSLMDGTLDSSYSRNPFTDVIQGYV     | 321 |
| QY | 121 | IPGMDSGLLGVCIGKRRIVVPHLGVGEGRGN-IPGSAVLVDFIDVDPNPSDTSI     | 179 |
| DB | 322 | IPGMDGQLQACIGERRITVPHLAYGNGTGDKIPGSAVLVDFVHVIDFHNPSDPVEI   | 381 |
| QY | 180 | TSHYKPPD-CSVLKSGDYLKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG | 238 |
| DB | 382 | KTLSPENCNETSKIGDFIRHYNCSLDGTLLFSSHDEYEAPOEITLGANKVIEGLDRG  | 441 |
| QY | 239 | LRMCVGEKRTVLIIPHLGVBAGVDEPGSAVLVDFIDELLELVAGLPEGYMIWNGEV   | 298 |
| DB | 442 | LQMGCVGERQLIVPPLAHGANGARG-VPGSAVLVFEVLVSREDGLPTGYLFVWYQDP  | 500 |
| QY | 299 | SPNLFREIN-----KVTFECCPFVSMRWYPEGRGOL-PQDSNDSPPADL          | 342 |
| DB | 501 | STSLFEDMDLNDKGEVPPPEFSFIKAQVN-----BKGKLMFGQDDPKTISDM       | 549 |

RESULT 2

T42709

Df   89 IAMEGVCVGEQRKVIIPPGQFDEDD-DEVEGKETLYYFFVELKSIFRPFGAKWITDGG 147

Qy 177 ISITHYKPDPDCSVLSKKGDYLKYHYNASILLDTLLSDTNLKGTYNIVLGSGGVVLGM D 236  
       ::                :  
Db 148 VHIHTHEVEGTGAQAAGDLTHQQYTNLLEDGSFDSSWSRNPFPFKMGSGOVIKGMD 207  
       ::                :

Qy 237 MGLREWCVGKEKTVIIPIPHLGYEAGVDGVPGSVALVFDELLELV 283  
       ::                :  
Db 208 IAMEGCQCCKEKWKVIPPELAYENGPRPAIPGNISYLFDFSLSEKL 254  
       ::                :

RESULT 4

T27580  
hypothetical protein C5OF2.6 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C/Accession: T29780  
R/DU, Z., Le, T.T.  
submitted to the EMBL Data Library, November 1996  
A/Description: The sequence of C. elegans cosmid C5OF2.  
A/Reference number: Z20684  
A/Accession: T29780  
A/Status: preliminary;  
A/Molecule type: DNA  
A/Residues: 1-264 <DUZ>  
A/Cross-references: EMBL,U08445; PIDN:AAB37799.1; GSPDB:GN00019; CESP:C5OF2.6  
A/Experimental source: strain Bristol N2; clone C5OF2  
C/Genetics:  
A/Gene: CESP:C5OF2.6  
A/Map position: 1  
A/Introns: 75/2; 205/3  
C/Superfamily: BKBP-type peptidyldiolyl isomerase homology  
F:50\_96/Domain: BKBP-type peptidyldiolyl isomerase homology <Ppil>  
F:171-218/Domain: BKBP-type peptidyldiolyl isomerase homology <Ppi2>

Query Match 16.3%; Score 344; DB 2; Length 264;  
Best Local Similarity 33.9%; Pred. No. 7.5e-21;  
Matches 80; Conservative 45; Mismatches 95; Indels 16; Gaps

Qy 63 KDSISIENKW---PENCERISQSQGFRLRYHYNGTLLDGTLPDFSSYSNRFTDYTGQG 118  
       |||:|||            |||            |||            |||||: : : ||  
Db 25 KDDEGLEKITRIPIKAECPKPSQDVLDQWKUSDKOGKETGSFNK-KPYTFILGKG 83  
       |||:|||            |||            |||            |||||: : : ||

Qy 119 YVIPQMDEGLLGVCTIGERRIYVPPHLGYGBEG--RGNI PGSAVLFDIHVIDFH----- 171  
       |||:|||            |||            |||            |||: : : |  
Db 84 QVIPMERAMTCMCKGKERKVIPGNLFGDGKRERNIDKDQTLYTVQLVDLFRAVPG 143  
       |||:|||            |||            |||            |||: : : |

Qy 172 ---NPSDISITSYHK-PPDCSVLSKGDYLKYHNASILLDTLLSDTNLKGTYNIVLG 227  
       |||:|||            |||            |||            |||: : : |

Db 144 EKWTTDGEIVTEQHDKEDCKSKSGDTIRHQVVLIHLEDGTFVDSFSRNAPFIPLKN 203  
       |||:|||            |||            |||            |||: : : |

Qy\* 228 SGQVVLGMDMGLREMCGVKERTVIIPPHLGYCEAGVDGVPGSVALVFDELLELV 283  
       |||:|||            |||            |||            |||: : : |

Db 204 NNEVIKNDIAMTGWCEGRQVIPSDFGYGDDGEAPAIPGKARLYFDITLEKLI 259  
       |||:|||            |||            |||            |||: ~::~~

RESULT 5

T27586  
hypothetical protein ZC455.10 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C/Accession: T27586  
R/Lighting, J.  
submitted to the EMBL Data Library, June 1996  
A/Reference number: Z20390  
A/Accession: T27586  
A/Status: preliminary;  
A/Molecule type: DNA  
A/Residues: 1-259 <WII>  
A/Cross-references: EMBL,Z75554; PIDN:CAA99959.2; GSPDB:GN00023; CESP:ZC455.10  
A/Experimental source: Clone ZC455  
C/Genetics:  
A/Gene: CESP:ZC455.10





QY 178 SITSHYK-PPDCSVLSKKGYLVKYNASLLDGTLLDSTWNLGKTYNIVLGGQVVLGMD 236  
Db 148 QDQIHKIEADCKKAEAGKIKYQYVLRLEDNTL-----EVIDGMD 189  
QY 237 MGLREMCVGEKRTVTPHPLHGKYGAGVDGPGSAVLVFDIELLELV 283  
Db 190 IAMDGMCEGERRRWWIPSEYGYGSGSPPEIPGGARLVFEIVLEKLV 236

## RESULT 9

S46228  
A:Title: peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus  
N:Alternate names: fkbB protein  
C:Species: Streptomyces chrysomallus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S46228  
R:Pahl, A.; Keller, U.  
EMBO J. 13, 3472-3480, 1994  
A:Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FKS  
A:Reference number: S46227; MUID:94341259; PMID:8062824  
A:Accession: S46228  
A:Molecule type: DNA  
A:Residues: 1-311 <PAH>  
A:Cross-references: GB:Z34523; NID:9535270; PIDN:CAA84280.1; PID:G633644  
A:Experimental source: ATCC 11523  
C:Genetics:  
A:Gene: fkbB  
C:Superfamily: peptidylprolyl isomerase FKBP33; BKBP-type peptidylprolyl isomerase homol  
C:Keywords: blocked amino end; cis-trans-isomerase; lipoprotein  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-311/Product: peptidylprolyl isomerase FKBP-33 #status predicted <MAT>  
F:77-125/Domain: BKBP-type peptidylprolyl isomerase homology <PP11>  
F:224-271/Domain: BKBP-type peptidylprolyl isomerase homology <PP12>  
F:19/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted  
F:19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted

Query Match 12.8%; Score 269.5; DB 1; Length 311;  
Best Local Similarity 27.6%; Pred. No. 1.3e-14;  
Matches 84; Conservative 51; Mismatches 98; Indels 71; Gaps 11;  
QY 18 GMCVGEKRIITPPFLAYGSDGDKIPGQASLVDFVALLDLHNPDKSISIEKVVPPNC 77  
Db 41 GAKFGEK-----PTLSKGS-GD-----PPKE--LKTDVISEGD 70  
QY 78 ERISQSGDFLRHYNGTLLDGTLL-FDSSYSNRRTFTYIGQYVTPGMDEGLLGVCIGEK 136  
Db 71 GAKLKNQDAIQNVLLGQAWSTKPFDFNSDKQKQFDLTGAGMVIQGWDKGLVGQKVS 130  
QY 137 RRIVVPHLYGGEGRGNIPGSVAVLVFDIHI----- 168  
Db 131 VELVIPPGLYGGQGGDIKENATLVFVVDILKATQIPASAKGTEVAQDNVDLPKVGKVT 190  
QY 169 DFHNPSDSI-----SITSHYKPPDCSVLSKKGDKYLVKYNASLLDGTLL-LDSTWNLGK 220  
Db 191 DGKAPTWTIPKSDPPKPKLVSNVLESDEGVVVKESDSVVNVVGMWKAKAFDNFTYTTGK 250  
QY 221 TYNIVLGGQVLL-GMDMGLREMCVGEKRTVTPHPLHGKYGAGVDGPGSAVLVFDIEL 279  
Db 251 TQTFPL--SQVTLKGLKNGLIDKKVGSRLVLTVPDQAFGQDQQA-IPKNSLTVFAVDI 307  
QY 280 LEIV 283  
Db 308 LAKV 311

## RESULT 10

T12090  
A:Title: probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15 precursor - fava bean  
N:Alternate names: FK506-binding protein; immunophilin; rapamycin-binding protein  
C:Species: Vicia faba (fava bean)  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 21-Jul-2000  
C:Accession: T12090  
R:Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.

Proc. Natl. Acad. Sci. U.S.A. 93, 6964-6969, 1996  
A:Title: Molecular characterization of a FKBP-type immunophilin from higher plants.  
A:Reference number: Z17411; MUID:96293457; PMID:8692927  
A:Accession: T12090  
A:Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: mRNA  
A:Residues: 1-151 <LUA>  
A:Cross-references: EMBL:U52045; NID:G1272409; PIDN:AAC49392.1; PID:G1272410  
C:Genetics:  
A:Gene: FKBP15

A:Note: inhibited by immunosuppressant drugs FK506 and rapamycin  
C:Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase  
C:Keywords: cis-trans-isomerase; cyclosporin A binding; immunoregulation  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-151/Product: peptidylprolyl isomerase FKBP15 #status predicted <MAT>  
F:49-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 12.8%; Score 269; DB 2; Length 151;  
Best Local Similarity 42.1%; Pred. No. 5.3e-15;  
Matches 56; Conservative 24; Mismatches 45; Indels 8; Gaps 3;  
QY 50 LVFDV-----ALLDLHNPDK--SISIEKVVPPNCERISQSGDFLRHYNGTLLDGTLLFD 102  
Db 8 LIPTIFIIASALVAKSAADVTELQIGVKYKPAQSCVQAQKDKVKVHYRGKLTGDTVFD 67  
QY 103 SSYSNRRTFTYIGQYVTPGMDEGLLGVCIGEKRTVTPHPLHGKYGEGR-GNIPGSVAVL 161  
Db 68 SSFERNSPIDFELGGQVIRKQWGLGMLGKGRKLIKIPAKLGYGEGSPPTIPGGATL 127  
QY 162 VPDHIVIDHNPS 174  
Db 128 IFDTLGVNDKS 140

## RESULT 11

S71238  
A:Title: probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliana  
N:Alternate names: FK-binding protein 15-2; immunophilin  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: S71238  
R:Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.  
submitted to the EMBL Data Library, March 1996  
A:Description: Molecular characterization of a FKBP-type immunophilin from higher pl  
A:Reference number: S71238  
A:Accession: S71238  
A:Molecule type: mRNA  
A:Residues: 1-163 <LUA>  
A:Cross-references: EMBL:U52047; NID:G1272407; PIDN:AAC49391.1; PID:G1272408  
C:Genetics:  
A:Gene: FKBP15-2

C:Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase  
C:Keywords: cis-trans-isomerase  
F:52-99/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 12.8%; Score 265.5; DB 2; Length 163;  
Best Local Similarity 48.1%; Pred. No. 1.1e-14;  
Matches 50; Conservative 17; Mismatches 36; Indels 1; Gaps 1;  
QY 66 ISTENKVVPPNCERISQSGDFLRHYNGTLLDGTLLFDSSYSNRRTFTYIGQYVTPGM 125  
Db 34 LQIGVAFKPTCVQAQKGTIKVHYRGKLTGDTVFDSSFERGDPFEFKLGGQVIGKWD 93  
QY 126 EGLLGVCIGEKRTVTPHPLHGKYGEGR-GNIPGSVAVLVFDIHI 168  
Db 94 QGLLGACVGEKRLKIPAKLGYGEGSPPTIPGGATLFDTELI 137

## RESULT 12

T26538  
A:Title: hypothetical protein Y18D10A.19b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 28-Jul-2000

Db 130 V 130

RESULT 14  
JT0748

FK506-binding protein - Botryllus schlosseri  
C;Species: Botryllus schlosseri  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JT0748; S40074  
R;Pancer, Z.; Gershon, H.; Rinkevich, B.  
Biochem. Biophys. Res. Commun. 197, 973-977, 1993  
A;Title: cDNA cloning of a putative protochordate FK506-binding protein.  
A;Reference number: JT0748; MUID:94092189; PMID:7505578  
A;Accession: JT0748  
A;Molecule type: mRNA  
A;Residues: 1-134 <PAN>  
A;Cross-references: EMBL:X76006; NID:g435470; PIDN:CAAS3594.1; PID:g435471  
C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomeras  
F;41-86/Domain: BKBP-type peptidylprolyl isomerase homology <PP1>

Query Match 12.2%; Score 256.5; DB 1; Length 134;  
Best Local Similarity 52.7%; Pred. No. 4.8e-14;  
Matches 49; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 77 CERISQSDFLRHYNGTLLDGTTFDSYSNRRTFTVIGQGYVPGWDEGLLGVCIGBK 136  
|||||  
DB 34 CERKSGSDVLDMHYYTGTLGDSKFSSRDTPFTFLGQGVYIKGWDKGLLMCEGER 93  
||||| :|||:  
QY 137 RRIIVPHLVYGERGR-GNIIPGSALVFEDIHI 168  
:||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:  
DB 94 RKLKIPSDMGYDRGSPKPPIGGATLPFDVELL 126  
::: :::

RESULT 15  
S72485

peptidylprolyl isomerase (EC 5.2.1.8) ROF1 - Arabidopsis thaliana  
N;Alternate names: FK506-binding protein; immunophilin; rotamase  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Jan-2001  
C;Accession: S72485; S72484  
R;Vuicich, V.A.; Gasser, C.S.  
Mol. Gen. Genet. 252, 510-517, 1996  
A;Title: Novel structure of a high molecular weight FK506 binding protein from Arabi  
A;Reference number: S72484; MUID:97071666; PMID:8914512  
A;Accession: S72485  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-551 <VVUC>  
A;Cross-references: EMBL:U57838; NID:gl373395; PIDN:AAB82062.1; PID:gl373396  
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, May 1996  
A;Accession: S72484  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-429 'v', 431-551 <VVUS>  
A;Cross-references: EMBL:U49453; NID:gl354206; PIDN:AAB82061.1; PID:gl354207  
C;Genetics:  
A;Gene: ROF1  
A;Introns: 62/1; 91/1; 178/1; 203/1; 295/1; 326/1; 384/3; 425/3; 474/3; 517/2  
C;Superfamily: peptidylprolyl isomerase ROF1; BKBP-type peptidylprolyl isomerase hom  
C;Keywords: calmodulin binding; cis-trans-isomerase  
F;57-104/Domain: BKBP-type peptidylprolyl isomerase homology <PP1>  
F;173-216/Domain: BKBP-type peptidylprolyl isomerase homology <PP12>  
F;190-339/Domain: BKBP-type peptidylprolyl isomerase homology <PP13>  
F;414-447/Domain: tetrahydrocysteine repeat homology <TT1>  
F;449-482/Domain: tetrahydrocysteine repeat homology <TT2>  
F;483-516/Domain: tetrahydrocysteine repeat homology <TT3>  
F;529-546/Region: calmodulin-binding #status predicted

Query Match 11.9%; Score 251.5; DB 1; Length 551;  
Best Local Similarity 30.9%; Pred. No. 8.9e-13;  
Matches 71; Conservative 34; Mismatches 88; Indels 37; Gaps 7;

Db 49 EGVETPEN-----GDEVEVHYTGTLDDGTYKFDSSRRDRAPEFFKFTLGQSQVVKGWDIGI 101  
Qy 129 LGVCIGEKRRIVVPHLYGEEGR-GNIPGSAVLVFDIHVIDFHNPSD-----SI 177  
Db 102 KTMKKGGENAVFTIPAELAYGESGSPPTIPANATLQFDVELLKWDSVKOICKDGGVFKIL 161  
Qy 178 SITSHYKPPDCSVLSKKGDYLYKHYNASLLDGTLLDSTWNLGKTYNI--VLGSGQVVLCM 235  
Db 162 AVGEKWENP-----KDLDEVLVVFEAKLEDGTV-----VGKSDGVFEFTVKDGHFPCPAL 209  
Qy 236 DMGLREMCVGEKRTVIIPPHLYGEAGV-----DGEVPGSAVLVFDIELL 280  
Db 210 TKAVKTMKGEKVLLTVKPOYGFGEKGPASAGEGAVPPNATLEINLELV 259

Search completed: April 26, 2003, 06:50:56  
Job time : 13.2714 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:55 ; Search time 6.91662 Seconds  
(without alignment)  
2326.688 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGEICGLIPGMDKGLGMC.....VNDPFLKLYFTNLNYFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 1022  | 48.5        | 581    | 1  | FKB3_MOUSE  |
| 2          | 283.5 | 13.5        | 559    | 1  | FKB7_WHEAT  |
| 3          | 251   | 11.9        | 140    | 1  | FKB2_MOUSE  |
| 4          | 237.5 | 11.3        | 135    | 1  | FKB2_YEAST  |
| 5          | 236.5 | 11.2        | 141    | 1  | FKB2_HUMAN  |
| 6          | 233.5 | 11.1        | 217    | 1  | FK21_NEUCR  |
| 7          | 208.5 | 9.9         | 120    | 1  | FKBP_NEUCR  |
| 8          | 195   | 9.3         | 456    | 1  | FKB5_MOUSE  |
| 9          | 194   | 9.2         | 208    | 1  | FKB3_HUMAN  |
| 10         | 193   | 9.2         | 208    | 1  | FKB3_ARATH  |
| 11         | 190   | 9.0         | 268    | 1  | FKB4_AERHY  |
| 12         | 189   | 9.0         | 457    | 1  | FKB4_RABIT  |
| 13         | 188   | 8.9         | 114    | 1  | FKBP_YEAST  |
| 14         | 188   | 8.9         | 458    | 1  | FKB4_HUMAN  |
| 15         | 184.5 | 8.8         | 108    | 1  | FKB1_DROME  |
| 16         | 182   | 8.6         | 112    | 1  | FKBP_SCHPO  |
| 17         | 177   | 8.4         | 107    | 1  | FKB1_BOVIN  |
| 18         | 176   | 8.4         | 241    | 1  | FKB1_HAEIN  |
| 19         | 175   | 8.3         | 457    | 1  | FKB4_MOUSE  |
| 20         | 173   | 8.2         | 107    | 1  | FKB1_HUMAN  |
| 21         | 172   | 8.2         | 107    | 1  | FKB1_RAT    |
| 22         | 171.5 | 8.1         | 109    | 1  | FKBP_NEIMA  |
| 23         | 171.5 | 8.1         | 270    | 1  | FKB4_ECOLI  |
| 24         | 169.5 | 8.0         | 109    | 1  | FKBP_NEIMB  |
| 25         | 169   | 8.0         | 107    | 1  | FKB1_MOUSE  |
| 26         | 164.5 | 7.8         | 205    | 1  | FKBB_ECOLI  |
| 27         | 164   | 7.8         | 241    | 1  | FKB4_BUCAL  |
| 28         | 161   | 7.6         | 107    | 1  | FKB1_XENLA  |
| 29         | 161   | 7.6         | 107    | 1  | FKB3_RAT    |
| 30         | 161   | 7.6         | 224    | 1  | FKB3_BOVIN  |
| 31         | 161   | 7.6         | 411    | 1  | FKB3_YEAST  |
| 32         | 160.5 | 7.6         | 224    | 1  | FKB3_MOUSE  |
| 33         | 160   | 7.6         | 107    | 1  | FKBB_HUMAN  |

#### RESULT 1

| ID | FKBX_MOUSE   | STANDARD; | PRT; | 581 AA. |
|----|--|-----------|------|---------|
| AC | Q61576;  |           |      |         |
| DT | 30-MAY-2000 (Rel. 39, Created)   |           |      |         |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update)  |           |      |         |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update)  |           |      |         |
| DE | 65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP65) (FKBPRP)  |           |      |         |
| DE | (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)  |           |      |         |
| DE | (Immunophilin FKBP65).   |           |      |         |
| GN | FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP.   |           |      |         |
| OS | Mus musculus (Mouse).  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |           |      |         |
| OX | NCBI_TaxID=10090;  |           |      |         |
| RN | [1]_SEQUENCE FROM N.A.   |           |      |         |
| RP | STRAIN=JUB6; TISSUE=Epidermis;   |           |      |         |
| RC | MEDLINE=94117013; PubMed7507077;   |           |      |         |
| RA | Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;   |           |      |         |
| RT | "Sequence and localization of a novel FK506-binding protein to mouse   |           |      |         |
| RT | chromosome 11";  |           |      |         |
| RL | Genomics 18:407-409(1993).   |           |      |         |
| RN | [2]  |           |      |         |
| RP | SEQUENCE FROM N.A., AND CHARACTERIZATION.  |           |      |         |
| RX | MEDLINE=96094328; PubMed7493967;   |           |      |         |
| RA | Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;   |           |      |         |
| RT | "Molecular cloning, DNA sequence analysis, and biochemical   |           |      |         |
| RT | characterization of a novel 65-kDa FK506-binding protein (FKBP65).";   |           |      |         |
| RL | J. Biol. Chem. 270:29336-29341(1995).  |           |      |         |
| CC | -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING  |           |      |         |
| CC | PROTEIN SYNTHESIS.   |           |      |         |
| CC | -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  |           |      |         |
| CC | PEPTIDE BONDS IN OLIGOPEPTIDES.  |           |      |         |
| CC | -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT  |           |      |         |
| CC | BY CYCLOSPORINE A.   |           |      |         |
| CC | -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL).   |           |      |         |
| CC | -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN  |           |      |         |
| CC | AND TESTIS.  |           |      |         |
| CC | -!- PTM: GLYCOSYLATED AND PHOSPHORYLATED.  |           |      |         |
| CC | -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4   |           |      |         |
| CC | FKBP-LIKE DOMAINS.   |           |      |         |
| CC | -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  |           |      |         |
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| CC | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |           |      |         |
| CC | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |           |      |         |
| DR | EMBL; L07063; AAC37678.1; --   |           |      |         |
| DR | HSSP; P20081; 1YAT.  |           |      |         |
| DR | MGI; MGI:104769; FKBP6.  |           |      |         |
| DR | InterPro; IPR002048; EF-hand.  |           |      |         |

O46638 oryctolagus  
Q00688 homo sapien  
P28725 streptomyce  
Q06205 saccharomyc  
P26623 chlamydia t  
P54397 drosophila  
P28870 candida alb  
O74191 schizosacch  
Q92703 chlamydia p  
P42458 corynebacte  
Q26486 spodoptera  
Q9pjki chlamydia m

```

DR InterPro: IPR000886; ER target.
DR InterPro: IPR001179; FKBP_PPIASE.
DR Pfam: PF00036; efhand; 2.
DR Pfam: PF00254; FKBP; 4.
DR SMART: SM00054; EFH; 2.
DR PROSITE: PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE: PS00454; FKBP_PPIASE 2; 1.
DR PROSITE: PS00059; FKBP_PPIASE 3; 4.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00018; EF_HAND; 1.
KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 33
FT CHAIN 34 581
FT DOMAIN 54 146
FT DOMAIN 179 258
FT DOMAIN 291 370
FT DOMAIN 389 482
FT CA_BIND 509 520
FT CA_BIND 554 565
FT CARBOHYD 69 69
FT CARBOHYD 181 181
FT CARBOHYD 293 293
FT CARBOHYD 309 309
FT CARBOHYD 351 351
FT CARBOHYD 392 392
FT CARBOHYD 406 406
FT SITE 578 581
SQ SEQUENCE 581 AA; 64669 MW; 1B51B3032089F555 CRC64;

Query Match 48.5%; Score 1022; DB 1; Length 581;
Best Local Similarity 55.8%; Pred. No. 3.1e-78;
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

QY 1 TYGEIGWLLIPGMKGLGCMVGEKRIITIPFLAYGDEGDKDIPQASLVFDVALLDLH 60
Db 202 TYIGSWLLKGMDOGLGCMVGEKRIITIPFLAYGDEGDKDIPQASLVFDVALLDLH 261
QY 61 NPKDTSIENKVVPCNERISQSGDFLRHYNGTLLDGTFLDSSYSNRRTFTDYGQYV 120
Db 262 NPKDTVQLETLELPQGVRRVAVAGDFWRYHNGSLMDGTFLDSSYSNRHNTITVGGYI 321
QY 121 IPGMDGLLGVCIGEKRIIVPHLGYGEGRGN-IPGSVAVLFDIHDVFNHPSDSISI 179
Db 322 IPGMDQGLQACIGERRRITVPPLAHGANG-IPGSVAVLFDVHVDHFNHPSDPVEI 381
QY 180 TSHYKPPD-CVLSKKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238
Db 382 KTLSPENCNETSKIGDFIRYHNCSLDGTFLFSSHDEYAPQEIITLGANKVIEGLDRG 441
QY 239 LREMVCGEKRTVITPPHLGYGEAGVGEVPGSAVLVFDIIBELVAGLPBGYFIWNGEV 298
Db 442 LQCMCVGERRLIVPHLHAGANG-VPGSVAVLFEVELVREDGLPTGYLFWVQDP 500
QY 299 SPNLFEIN-----KVTFFCPCFVSWRWYPPGRQL-PQDSNDSPPADL 342
Db 501 STSLFEDMDLNKDGVPPEFFSFIFKAQVN-----EGKRLMFGQDPDKTISDM 549

RESULT 2
FKB7_WHEAT
ID FKB7_WHEAT STANDARD; PRT; 559 AA.
AC Q43207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
DE isomerase) (Cyclophilin) (PPIase).
GN FKB70.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.

```

```

OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATIR; TISSUE=Root tip;
RA Oshra B., Breiman A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
CC FKBP-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC
CC EMBL; X86903; CAA60505.1; -.
CC HSSP; P27124; 1ROT.
CC InterPro: IPR001179; FKBP_PPIASE.
CC InterPro: IPR001440; TPR.
CC Pfam; PF00254; FKBP; 3.
CC Pfam; PF00515; TPR; 3.
CC SMART; SM00028; TPR; 3.
CC PROSITE; PS00453; FKBP_PPIASE 1; 1.
CC PROSITE; PS00454; FKBP_PPIASE 2; 3.
CC PROSITE; PS00059; FKBP_PPIASE 3; 3.
KW Isomerase; Rotamase; Repeat; TPR repeat; Heat shock;
KW Calmodulin-binding.
FT DOMAIN 60 148
FT DOMAIN 176 265
FT DOMAIN 293 384
FT REPEAT 401 434
FT REPEAT 450 483
FT REPEAT 484 517
FT REPEAT 517 517
SQ SEQUENCE 559 AA; 62056 MW; 5C5DAE70D716B541 CRC64;

Query Match 13.5%; Score 283.5; DB 1; Length 559;
Best Local Similarity 29.5%; Pred. No. 3.3e-16;
Matches 80; Conservative 43; Mismatches 107; Indels 41; Gaps 8;

QY 40 DGKDIPQASLVFDVALLDL---HNPKDTSIENKVVPCNER-----ISQSGDF 86
Db 3 DDFDIPAGDDMMGDMGDFGAGPGMKVGEENEIGKQGLKKLLKEGEGWDTPEVGDE 62
QY 87 LRHYNGTLLDGTFLDSSYSNRRTFTDYGQYVPGMDGLLGVCIGEKRIIVPPHLG 146
Db 63 VEVHYTGTLGKFKFSRDRDFTFKLGGQGVIKGWDQGIKTMKGGENALFTTPELA 122
QY 147 YGEGR-NTIPGSVAVLFDIHDVFNHPSDSISITSHYKPPDCSVLSKKGD----- 196
Db 123 YGESGSPPTIPANATLQFDVELLSWTSVRDTAKGGIFK-----ILKEGDKWENKDDP 177
QY 197 --YLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLEMCVGEKRTVI 254
Db 178 EVFVK--YEARLEDGTIVSKS---EGVEFTVKDGHLCALAKAVKTMKGEKVLAVKP 231
QY 255 HLGVE-----AGVDGEVPGSAVLVFDIELL 280
Db 232 QYFGEMGRPAAGEGGAVPPNASLVIDELV 262

RESULT 3
FKB2_MOUSE
ID FKB2_MOUSE STANDARD; PRT; 140 AA.
AC F45878;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

```



Db 13 STILAGSLDL-----EIGIKRIPVEDCLIKAMPQDKVKVHYTGSLLSGTVPDSSYSR 67

Qy 108 NRTFDYIQQGVVPGWDEGLLGVICIGEKRRIVVPHLGVGEG- RGNIPGSVAVLFDIH 166

Db 68 GSPIAFELGVGRVIGWQDQVAGCMGCKRKLQIPSSLAYGERGVPGVIPPSSADLVFDE 127

Qy 167 VID 169

Db 128 LVD 130

RESULT 5

FKB2 HUMAN STANDARD; PRT; 141 AA.

ID\_FKB2\_HUMAN

AC P26885

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).

GN FKBP2 OR FKBP13

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Colon carcinoma;

RA MEDLINE=91319747; PubMed=1713687;

RX Jin Y.-J., Albers M.W., Lane W.S., Bierter B.E., Schreiber S.L., Burakoff S.J.

RT "Molecular cloning of a membrane-associated human FK506- and rapamycin-binding protein, FKBP-13.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681 (1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93112052; PubMed=1281998;

RA Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.; "Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13.";

RT Biochem. Biophys. Res. Commun. 189:819-823 (1992).

RL

CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).

CC -!- TISSUE SPECIFICITY: T-CELLS AND THYMUS.

CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

CC

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CC

DR EMBL; M65128; AAA58473.1; -.

DR EMBL; M75099; AAA36563.1; -.

DR F01; JC1365; JC1365.

DR HSSP; Q00688; 1PBK.

DR Genew; HGNC:3718; FKBP2.

DR MIM; 186946; -.

DR InterPro; IPR001179; FKBP\_PPIase.

DR Pfam; PF00254; FKBP; 1.

DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.

DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.

DR PROSITE; PS00059; FKBP\_PPIASE\_3; 1.

DR Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.

KW SIGNAL

FT CHAIN 1 21 FK506-BINDING PROTEIN.

FT SITE 22 141 PREVENT SECRETION FROM ER (POTENTIAL).

FT

FT VARIANT 21 21 S -> TA.

FT /FTId=VAR\_006410.

FT T -> A.

FT /FTId=VAR\_006411.

FT Y -> C.

FT /FTId=VAR\_006412.

SQ SEQUENCE 141 AA; 15654 MW; 9F4751CA7D82D064 CRC64;

Query Match 11.2%; Score 236.5; DB 1; Length 141;

Best Local Similarity 46.7%; Pred. No. 4.9e-13;

Matches 50; Conservative 18; Mismatches 36; Indels 3; Gaps 2;

Qy 63 KDSISIEKVVPCNERISQSGDFLRVHYNGTLLDGLTFLDSSYSRNRFTDYIGGVYIP 122

Db 29 KLIQGVKKRV--DHCPIKSKGKGVLMHYTKLEDTGFEFSSLPQNFVPSLGTQGVIK 86

Qy 123 GNDGELLGVICIGEKRRIVVPHLGVGEGR-GNIPGSVAVLFDIHVI 168

Db 87 GWDQGLGVGEGEKRLVIPSELGYGERGAPKIPGGATLVFEVELL 133

RESULT 6

FK21 NEUCR STANDARD; PRT; 217 AA.

ID\_FK21\_NEUCR

AC O60046;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FK506-binding protein precursor (FKBP-21) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).

GN FKBP-21.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.

OX NCBI\_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=74-OR23-1A;

RA Soleschield B., Tropshug M.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).

CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

CC

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CC

DR EMBL; AJ006297; CAA06962.1; -.

DR HSSP; Q00688; 1PBK.

DR InterPro; IPR000886; ER target.

DR InterPro; IPR001179; FKBP\_PPIase.

DR Pfam; PF00254; FKBP; 1.

DR PROSITE; PS00453; FKBP\_PPIASE\_1; FALSE\_NEG.

DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.

DR PROSITE; PS00059; FKBP\_PPIASE\_3; 1.

DR PROSITE; PS00014; ER\_TARGET; 1.

DR Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.

KW SIGNAL

FT CHAIN 1 20 POTENTIAL.

FT SITE 21 217 FK506-BINDING PROTEIN.

FT CHAIN 214 217 PREVENT SECRETION FROM ER (POTENTIAL).

SQ SEQUENCE 217 AA; 22915 MW; 72313067521BCDAF CRC64;

Query Match 11.1%; Score 233.5; DB 1; Length 217;

Best Local Similarity 46.4%; Pred. No. 1.5e-12;

Matches 45; Conservative 15; Mismatches 36; Indels 1; Gaps 1;







OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and TAC clones.";  
 RL DNA Res. 5:203-216(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RT "Riken Arabidopsis full length cDNA clones (RAFTs) sequenced by the  
 RT SSP consortium (Salk/Stanford/PGEC).";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 101-176 FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Kolkisaoglu U., Billion K., Eckhoff A., Moeller A., Saal B.,  
 RA Wanke D., Schulz B.;  
 RT "Structure and evolution of FKBP-like genes in Arabidopsis.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 80-99.  
 RC STRAIN=cv. Columbia;  
 RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;  
 RL Submitted (JAN-2000) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes  
 CC the cis-trans isomerization of proline imidic peptide bonds in  
 CC oligopeptides (by similarity).  
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline  
 CC (omega=0).  
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AB012245; BAB09210.1; -  
 CC EMBL; AY065047; AAL57682.1; -  
 CC EMBL; AJ242483; CAB64723.1; -  
 CC HSSP; P20081.1VAT.  
 CC InterPro; IPR001179; FKBP\_PPIase.  
 CC Pfam; PF00254; FKBP; 1.  
 CC ProDom; PD001516; FKBP\_Nterm; 1.  
 CC PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 CC PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 CC PROSITE; PS00059; FKBP\_PPIASE\_3; 1.  
 CC Isomerase; Rotamase; Chloroplast; Thylakoid; Transit peptide.  
 KW TRANSIT ? ? CHLOROPLAST (POTENTIAL).  
 FT TRANSIT ? 79  
 FT CHAIN 80 208  
 FT PROBABLE FKBP-TYPE PEPTIDYL-PROLYL CIS-  
 FT TRANS ISOMERASE 3.  
 FT SEQUENCE 208 AA; 22039 MW; 4E6640FE7955A48F CRC64;  
 SQ  
 Query Match 9.2%; Score 193; DB 1; Length 208;  
 Best Local Similarity 35.3%; Pred. No. 3.7e-09;  
 Matches 49; Conservative 23; Mismatches 45; Indels 22; Gaps 5;  
 Qy 52 FDVALLD-LHNPKDSISNKKVVPEN---CERI-----SQSGDFLRHYNGTLLDGTFL 101  
 Db 67 FSIGLDNLVSALETSCFSFSPSGLAFCDKVGVGPEAVKQLIKAHVGLKNGKVF 126  
 Qy 102 DSSYSRNRFTDYIGGYVPGMDEGLLG-----VCIGEKRIIVVPHLYGEEGRG-- 153  
 Db 127 DSSYNRGKPLTPRIGVGEVIKGDQILGSDGIPPLMTGKRTLRIPPELAYDGRGAGCK 186

QY 154 ----NIPSAVLVFDIHI 168  
 Db 187 GGSCLIPPASVLLFDIEYI 205  
 RESULT 11  
 FKBP\_AERHY STANDARD; PRT; 268 AA.  
 ID O08437;  
 AC 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE FKBP-type peptidyl-prolyl cis-trans isomerase fkpa precursor  
 DE (EC 5.2.1.8) (PPIase) (Rotamase).  
 GN FKPA.  
 OS Aeromonas hydrophila.  
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;  
 OC Aeromonas.  
 OX NCBI\_TaxID=644;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A6;  
 RX MEDLINE=97315206; PubMed=9171380;  
 RA Wong C.Y.F., Heuzenroeder M.W., Quinn D.M., Flower R.L.P.;  
 RT "Cloning and characterization of two immunophilin-like genes, ilpa and  
 RT fkpa, on a single 3.9-kilobase fragment of Aeromonas hydrophila  
 RT genomic DNA.";  
 RL J. Bacteriol. 179:3397-3403(1997).  
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKPA  
 CC PROBABLY ACTS IN THE FOLDING OF EXTRACYTOSOLIC PROTEINS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC  
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 CC  
 CC EMBL; U56832; AAC45362.1; -  
 CC HSSP; P20071.1FKJ.  
 CC InterPro; IPR000774; FKBP\_Nterm.  
 CC InterPro; IPR001179; FKBP\_PPIase.  
 CC Pfam; PF00254; FKBP; 1.  
 CC Pfam; PF01346; FKBP\_N; 1.  
 CC ProDom; PD001516; FKBP\_Nterm; 1.  
 CC PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 CC PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 CC PROSITE; PS00059; FKBP\_PPIASE\_3; 1.  
 CC Isomerase; Rotamase; Periplasmic; Signal.  
 KW SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 268  
 FT FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS  
 FT ISOMERASE FKPA.  
 FT DOMAIN 172 257  
 FT PPIASE, FKBP-TYPE.  
 FT SEQUENCE 268 AA; 28685 MW; 5E88D74A830BE3FA CRC64;  
 SQ  
 Query Match 9.0%; Score 190; DB 1; Length 268;  
 Best Local Similarity 43.3%; Pred. No. 9.1e-09;  
 Matches 39; Conservative 14; Mismatches 35; Indels 2; Gaps 1;  
 QY 85 DFLRYHYNGTLLDGTFLDSSYSRNRFTDYIGQYVPGMDEGLLGVCIGEKRIIVVPH 144  
 Db 173 DIVKHYTGTLTDTGTFDSSVDRGPATFPLNQ--VIPGWTEGVQLMPVGSFKFPLPSK 230  
 QY 145 LGVGEGRGNIPGSANVLVFDIHI 174  
 Db 231 LAYGEHAGSIPANANVLVFDVALLAIEKPA 260

| RESULT 13 |                              |  |
|-----------|------------------------------|--|
| ID        | FKBP YEAST                   | STANDARD; PRT; 114 AA.                   |
| AC        | P20081;                      |  |
| DTL       | 01-FEB-1991                  | (Rel. 17, Created)                       |
| DT        | 01-MAY-1991                  | (Rel. 18, Last sequence update)          |
| DT        | 15-JUL-1999                  | (Rel. 38, Last annotation update)        |
| DE        | FK506-binding protein [FKBP] | (Peptidyl-prolyl<br>cis-trans isomerase) |



RA Lipkpe J.A., Livingston D.J., Benasutti M.;  
 RT "Expression and characterization of human FKBP52, an immunophilin  
 RT that associates with the 90-kDa heat shock protein and is a component  
 RT of steroid receptor complexes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10974-10978(1992).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung, Lymph, and Uterus;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE OF 1-24, SUBUNIT, AND FUNCTION.  
 RC TISSUE=Thymus;  
 RX MEDLINE=92285692; PubMed=1376003;  
 RA Tai P.-K.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;  
 RT "Association of a 59-kilodalton immunophilin with the glucocorticoid  
 RT receptor complex.";  
 RL Science 256:1315-1318(1992).  
 [4]  
 RN SEQUENCE OF 1-20, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.  
 RC TISSUE=Lymphocytes;  
 RX MEDLINE=90335311; PubMed=2378870;  
 RA Sanchez E.R., Faber L.E., Henzel W.J., Pratt W.B.;  
 RT "The 56-59-kilodalton protein identified in untransformed steroid  
 RT receptor complexes is a unique protein that exists in cytosol in a  
 RT complex with both the 70- and 90-kilodalton heat shock proteins.";  
 RL Biochemistry 29:5145-5152(1990).  
 [5]  
 RN SEQUENCE OF 1-17.  
 RC TISSUE=T-cell;  
 RX MEDLINE=92147620; PubMed=1371107;  
 RA Yem A.W., Tomasselli A.G., Heinrikson R.L., Zurcher-Neely H.,  
 RA Ruff V.A., Johnson R.A., Deibel M.R. Jr.;  
 RT "The Hsp56 component of steroid receptor complexes binds to  
 RT immobilized FK506 and shows homology to FKBP-12 and FKBP-13.";  
 RL J. Biol. Chem. 267:2868-2871(1992).  
 CC -!- FUNCTION: Component of unactivated mammalian steroid receptor  
 CC complexes that sediment at 8-10 S. May have a rotamase activity.  
 CC May play a role in the intracellular trafficking of hetero-  
 CC oligomeric forms of steroid hormone receptors.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid  
 CC hormone receptor complexes. Also interacts with peroxisomal  
 CC phytanoyl-coA alpha-hydroxylase (PHYH).  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.  
 CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding  
 CC activity (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.

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 -----  
 DR EMBL; M88279; AAA36111.1; -;  
 DR EMBL; BC001786; AAH01786.1; -;  
 DR EMBL; BC002887; AAH02887.1; -;  
 DR EMBL; BC007924; AAH07924.1; -;  
 DR PIR; A46372; A46372.  
 DR HSSP; P27124; 1ROT.  
 DR Genew; HGNC:3720; FKBP4.  
 DR MIM; 600611; -;  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00254; FKBP; 2.  
 DR Pfam; PF00515; TPR; 3.

DR SMART; SM00028; TPR; 3.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 2.  
 DR PROSITE; PS00559; FKBP\_PPIASE\_3; 2.  
 KW Isomerase; Rotamase; Repeat; TPR repeat; Nuclear protein;  
 KW Phosphorylation.  
 FT INIT MET 0  
 FT DOMAIN 49 137 PPIASE, FKBP-TYPE 1.  
 FT DOMAIN 166 252 PPIASE, FKBP-TYPE 2.  
 FT REPEAT 269 302 TPR 1.  
 FT REPEAT 318 351 TPR 2.  
 FT REPEAT 353 385 TPR 3.  
 FT MOD\_RES 142 142 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).  
 FT CONFLICT 145 146 ED -> AR (IN REF. 2; AAH02887).  
 SQ SEQUENCE 458 AA; 51673 MW; 916B3B945C51634E CRC64;  
 Query Match 8.9%; Score 188; DB 1; Length 458;  
 Best Local Similarity 27.6%; Pred. No. 2.7e-08;  
 Matches 58; Conservative 36; Mismatches 92; Indels 24; Gaps 7;  
 QY 84 GDFLRHYNGTLDGTLFDSSYSRNRTFDYIGGYVPGMDGLGVCIGEKRRIVVPP 143  
 DB 49 GDRVFVHYTGWLLDGTGKFDSSLDKDKFSPDLGKGEVKAWDIAIATMKVGEVCHITCKP 108  
 QY 144 HLGYGEGR-GNIPGSAVLVFDIHVIDFH-----NPDSISI-----TSHYKPPDCSV 190  
 DB 109 EVAYSGAGSPKIPPNATLVFEVLFEGKEDLTEEDGGIIRIOTRGEYAKNEGAI 168  
 QY 191 LSKKGDYLYKHYNASLLDGTLLSTWNLGKTYNTVLGSGQVVLGMDMLGRLMVCVEKRTV 250  
 DB 169 VEVA---LEGYKDKLFDQREL--RFEIGENL-----DLPGYGLERAIQRMKEGHSIV 218  
 QY 251 IIPPHLGYGEAGVDG-EVPGSAVLVFDIEL 279  
 DB 219 YLKPSYAFSGVGKFKQIPPNALKEYLHL 248  
 RESULT 15  
 ID FKBP\_DROME STANDARD; PRT; 108 AA.  
 AC P48375;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 12 kDa FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans  
 DE isomerase) (PPIase) (EC 5.2.1.8) (Macrolide binding protein).  
 GN FK506-BP2 OR FKBP12.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S; TISSUE=Head;  
 RA Mounsey A.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,  
 RA Lechleider R.J., Martin J., Mangano T., Donahoe P.K.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC -----  
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DR EMBL; Z49079; CAA88904.1; -;  
DR EMBL; U41441; AAG11178.1; -;  
DR HSSP; P18203; 1PKL.  
DR FlyBase; FBgn013954; FK506-bp2.  
DR InterPro; IPR001179; FKBP\_PPIase.  
DR Pfam; PF00254; FKBP; 1.  
DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE; PS0059; FKBP\_PPIASE\_3; 1.  
KW isomerase; Rotamase.  
SQ SEQUENCE 108 AA; 11597 MW; 48BCF993AC8D350A CRC64;

Query Match 8.8%; Score 184.5; DB 1; Length 108;  
Best Local Similarity 37.8%; Pred. No. 8.1e-09;  
Matches 37; Conservative 19; Mismatches 41; Indels 1; Gaps 1;

Qy 72 VVPENCERISQSGDPLRYHYNGTLLDGTLDSSYSRNRTFTVIGQYVIPGMDEGLGV 131  
Db 8 IAPGDGSTYPKNGQVTVYHTTGLDGTGKFDSSRDNRNPFKFTIGKEVIRGWDGVAQL 67  
Qy 132 CIGEKRRIVVPPHLYGEGR-GNIPGSALVFDIHVI 168  
Db 68 SVQGSAKLICSPDYAYGSRGHPGVIPPNSTLTDFVELL 105

Search completed: April 26, 2003, 06:56:22  
Job time : 8.91662 secs





GenCore version 5.1.4.D5 4578  
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 34.1369 Seconds

(without alignments)  
2341.934 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGEIGWLIPGMKGLGMC.....VNDPFLKLYFTNLNYFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 1623   | 77.1        | 517    | 4  | Q95302      |
| 2          | 1585   | 75.3        | 570    | 11 | Q92247      |
| 3          | 1585   | 75.3        | 570    | 11 | Q8R386      |
| 4          | 1353   | 64.2        | 577    | 13 | Q9YIC3      |
| 5          | 1059.5 | 50.8        | 564    | 13 | Q9I8P8      |
| 6          | 1022   | 48.5        | 581    | 11 | Q8VHI1      |
| 7          | 1000.5 | 47.5        | 481    | 4  | Q9H6N5      |
| 8          | 1000.5 | 47.5        | 582    | 4  | Q9H3N3      |
| 9          | 1000.5 | 47.5        | 582    | 4  | Q96AY3      |
| 10         | 688    | 32.7        | 355    | 4  | Q9H6J3      |
| 11         | 572.5  | 27.2        | 262    | 4  | Q9UEF9      |
| 12         | 386    | 18.3        | 137    | 13 | Q98UD7      |
| 13         | 353.5  | 16.8        | 261    | 5  | O16309      |
| 14         | 344    | 16.3        | 264    | 5  | P91180      |
| 15         | 344    | 16.3        | 300    | 5  | Q95Q60      |
| 16         | 301.5  | 14.3        | 259    | 5  | Q23338      |

|    |       |      |     |    |        |
|----|-------|------|-----|----|--------|
| 17 | 287   | 13.6 | 216 | 5  | Q9V3V2 |
| 18 | 286.5 | 13.6 | 139 | 5  | Q20107 |
| 19 | 285   | 13.5 | 216 | 5  | Q9XZ54 |
| 20 | 275   | 13.1 | 138 | 5  | Q9VGK3 |
| 21 | 274   | 13.0 | 578 | 10 | Q9FJL3 |
| 22 | 272.5 | 12.9 | 209 | 5  | Q966Y5 |
| 23 | 269.5 | 12.8 | 312 | 2  | Q53919 |
| 24 | 269   | 12.8 | 151 | 10 | Q41649 |
| 25 | 265.5 | 12.6 | 163 | 10 | Q9FJL2 |
| 26 | 265.5 | 12.6 | 163 | 10 | Q38936 |
| 27 | 262   | 12.4 | 304 | 5  | Q9XW05 |
| 28 | 259   | 12.3 | 146 | 10 | Q38935 |
| 29 | 259   | 12.3 | 153 | 10 | Q9LSF4 |
| 30 | 256.5 | 12.2 | 134 | 5  | Q17280 |
| 31 | 251.5 | 11.9 | 551 | 10 | Q38931 |
| 32 | 251.5 | 11.9 | 551 | 10 | Q38949 |
| 33 | 251.5 | 11.9 | 555 | 10 | Q9LSF3 |
| 34 | 250.5 | 11.9 | 568 | 10 | O04843 |
| 35 | 247.5 | 11.8 | 142 | 4  | Q9BTS7 |
| 36 | 237.5 | 11.3 | 137 | 5  | Q96335 |
| 37 | 234.5 | 11.1 | 211 | 4  | Q9NMW8 |
| 38 | 227.5 | 10.8 | 119 | 13 | Q9DFL8 |
| 39 | 225.5 | 10.7 | 198 | 11 | Q9CRE4 |
| 40 | 225   | 10.7 | 222 | 4  | Q9Y6B0 |
| 41 | 225   | 10.7 | 222 | 4  | Q96DA4 |
| 42 | 223.5 | 10.6 | 189 | 11 | Q9D8P8 |
| 43 | 223.5 | 10.6 | 201 | 11 | Q9D1M7 |
| 44 | 221.5 | 10.5 | 201 | 4  | Q9NYL4 |
| 45 | 214.5 | 10.2 | 113 | 16 | Q9HXS4 |

## ALIGNMENTS

RESULT 1

Q95302 PRELIMINARY; PRT; 517 AA.

AC Q95302; Q96IJ9; Q96EX5;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE FK506 binding protein 9 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans

isomerase) (PPIase) (Rotamase) (Fragment).

GN FKBP9 OR FKBP63.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99453729; PubMed=10524204;

RA Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;

RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP

family.";

RL Biochim. Biophys. Acta 1446:295-307(1999).

RP [2]

SEQUENCE OF 317-517 FROM N.A.

RC TISSUE=KIDNEY, AND MUSCLE;

RA Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

CC -! FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING

CC -! PROTEIN SYNTHESIS.

CC -! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC -! PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -! ENZYME REGULATION: INHIBITED BY FK506 (BY SIMILARITY).

CC -! SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (BY SIMILARITY).

CC -! PTM: PHOSPHORYLATED (BY SIMILARITY).

CC -! SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4

CC -! FKBP-LIKE DOMAINS.

CC -! SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

DR EMBL; AF089745; AAC78853.1; -

DR EMBL; BC007443; AA07443.1; -

DR EMBL; BC011872; AA11872.1; -

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DR HSP; P20081; 1YAT.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001179; FKBP_PPIase.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00254; FKBP; 4.
DR SMART; SM00054; Eph; 2.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; 3.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
DR isomerase; Rotamase; Repeat; Glycoprotein; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 1
FT DOMAIN 1 86 PPIASE, FKBP-TYPE 1.
FT DOMAIN 105 198 PPIASE, FKBP-TYPE 2.
FT DOMAIN 216 309 PPIASE, FKBP-TYPE 3.
FT DOMAIN 328 421 PPIASE, FKBP-TYPE 4.
FT CA_BIND 439 467 EF-HAND 1 (POTENTIAL).
FT CA_BIND 484 510 EF-HAND 2 (POTENTIAL).
FT SITE 514 517 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 317 319 SIS -> HEG (IN REF. 2; AAH07443).
FT CONFLICT 514 514 H -> Q (IN REF. 2; AAH11872).
SQ SEQUENCE 517 AA; 57219 MW; 704FB0C9C44C74B CRC64;

Query Match 77.1%; Score 1623; DB 4; Length 517;
Best Local Similarity 99.0%; Pred. No. 5.6e-130;
Matches 305; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TYVEIGWLIPGMDKGLLGMVCGEKRIITIPPTLAYGDDGDKIPQASLVFDVALLDLH 60
Db 142 TYVGIGLWIPGMDKGLLGMVCGEKRIITIPPTLAYGDDGDKIPQASLVFDVALLDLH 201

Qy 61 NPKDSISIKVVPNCERISQSQDFLYHYNGTLLDGLTLDSSYSRNRRTDTYIGQGV 120
Db 202 NPKDSISIKVVPNCERISQSQDFLYHYNGTLLDGLTLDSSYSRNRRTDTYIGQGV 261

Qy 121 IPGMDGLGVCIGEKRIIVPPHLYGEGRGNIPGSALVFDIHVDHFNPSDSISIT 180
Db 262 IPGMDGLGVCIGEKRIIVPPHLYGEGRGNIPGSALVFDIHVDHFNPSDSISIT 321

Qy 181 SHYKPPDCSVLSKKGYLYKYHNASLLDGLTLDSTWNLGKTYNIVLGSQGVVLGMDMGLR 240
Db 322 SHYKPPDCSVLSKKGYLYKYHNASLLDGLTLDSTWNLGKTYNIVLGSQGVVLGMDMGLR 381

Qy 241 EMCVGEKRTVIIPHLGYGAGVDGEPVGSALVFDIELLELVAGLPEGYFVWNGEVSP 300
Db 382 EMCVGEKRTVIIPHLGYGAGVDGEPVGSALVFDIELLELVAGLPEGYFVWNGEVSP 441

Qy 301 NLFEEINK 308
Db 442 NLFEEIDK 449

RESULT 2
Q92247 PRELIMINARY; PRT; 570 AA.
AC Q92247; Q9JHX5; Q9CVMO;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE F506 binding protein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (FKBPp65RS).
GN* FKBP9 OR FKBP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A., ENZYME REGULATION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, DEVELOPMENTAL STAGE, AND CALCIUM-BINDING ACTIVITY.
RX MEDLINE=99453729; PubMed=10524204;
RT Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;
RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP
RT family.";
RL Biochim. Biophys. Acta 1446:295-307(1999).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=THYMUS;
RX PubMed=11710534;
RA Jo D., Lyu M.S., Cho S.-G., Park D., Kozak C.A., Kim M.G.;
RA "Identification and genetic mapping of the mouse Fkbp9 gene encoding a
RT new member of FK506-binding protein family.";
RT Mol. Cells 12:272-275(2001).
RN [3]
RP SEQUENCE OF 155-570 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
CC PROTEIN SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY FK506.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL
CC MUSCLE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN,
CC SPLEEN AND TESTIS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL DEVELOPMENTAL STAGES.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4
CC FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR EMBL; AF090334; AAC72964.1; -
DR EMBL; AF279263; AAF79215.1; -
DR EMBL; AK007499; BAB25071.1; -
DR HSP; P20081; 1YAT.
DR MGD; MGI:1350921; Fkbp9.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; Eph; 2.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; 3.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
DR isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 24
FT POTENTIAL.

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Db 260 NPKDGIITENQVLVPESECRRTQTGDFIRYHYNGTLLDGTLLFDSSYSRNRTYDTYVGKGV 319  
 Qy 121 IFGMEGLLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHVIDFHNPSDSISIT 180  
 Db 320 IAGMEGLLGVCIGEKRRIRIIPHLGYGEGRGKIPGSAVLVFDIHVADEFNPSDSVSI 379  
 Qy 181 SHYKPPDCSVLSKGGDYLYKHYNASLL--DGTLLDSTNGLKTYNIVLGSQVVLGMDM 237  
 Db 380 VNYKPSNCSLLSKGGDYLYKHYNASLLGWSASLDTSW---QDLQSSGSGQVVLGMDM 436  
 Qy 238 GLREMCVGEKRTVIIPHLGYGAGVDGVP GSAVLVFDIELLELVAGLPEGYMFIWNGE 297  
 Db 437 GLQDMCVGERRTVIIPHLGYGEGVEGVP GSAVLVFDIELLELVAGLPEGYMFIWNGE 496  
 Qy 298 VSPNLFEEINK 308  
 Db 497 VSPNLFEEIDQ 507

## RESULT 5

Q918P8 PRELIMINARY; PRT; 564 AA.  
 AC Q918P8;  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE FK506-binding protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2032564; PubMed=10842073;  
 RA Spokony R., Saint-Jeannet J.-P.;  
 RT "Xenopus FK 506-binding protein, a novel immunophilin expressed during  
 early development.";  
 RL Mech. Dev. 94:205-208(2000).  
 DR EMBL; AF232672; AAF35906.1; -.  
 DR HSSP; P20081; 1YAT.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR Pfam; PF00036; ehand; 2.  
 DR Pfam; PF00254; FKBP; 4.  
 DR SMART; SM00054; EFh; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 1.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; UNKNOWN\_2.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 4.  
 SQ SEQUENCE 564 AA; 62643 MW; 15312365BF1E43CF CRC64;

Query Match 50.8%; Score 1069.5; DB 13; Length 564;  
 Best Local Similarity 58.5%; Pred. No. 1e-82;  
 Matches 207; Conservative 48; Mismatches 80; Indels 19; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLLGMVCGEKRIITIPFLAYGEDGDKDIPGQASLVFDVALLDLH 60  
 Db 186 TVVGSGLWIKGMDGLGMLGMCAGKRRITIPFLAYGEKGYGTIIPQAQSLVFHVLLIDFH 245  
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLRYHYNGTLLDGTLLFDSSYSRNRTFTYIGQYV 120  
 Db 246 NPKDGIITVQNVQVCKKAVTGDYRYHYNGTLLDGTLLFDSSYSRNRTFTYIGMIV 305  
 Qy 121 IFGMEGLLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHVIDFHNPSDSIS 179  
 Db 306 ISGMDAGLQVCVGEKRRIRIIPHLGYGEGSGNSIPGSAVLVFDIHVIDFHNPSDVI 365  
 Qy 180 TSHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTNGLKTYNIVLGSQVVLGMDMGL 239  
 Db 366 FVMHKPDSNTTSKGGDFIKYHNCNMLDGTLLFSSHEYETPQQVTLGSSKVGIEGLDTGL 425

Qy 240 REMCVGEKRTVIIPHLGYGAGVDGVP GSAVLVFDIELLELVAGLPEGYMFIWNGEVS 299  
 Db 426 LQMCVGERRTVIIPHLAHGEGSARG-VPPSAVLKFDLELLHIEGIPDGLFVWLQDTP 484  
 Qy 300 PNLFE-----EINKVTF--FCCPFVSWRRWYPEGQG-LPQDSNDSPPADL 342  
 Db 485 ENLFEMLDLKNGEVPEEFDFLKAQVS-----EGKGRFLPGVDREKSIADM 532

## RESULT 6

Q8VHI1 PRELIMINARY; PRT; 581 AA.  
 AC Q8VHI1;  
 DT 01-MAR-2002 (TREMELrel. 20, Created)  
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)  
 DE 65 kDa FK506-binding protein.  
 GN FKBP10.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Patterson C.E., Gao J., Rooney A.P., Davis E.C.;  
 RT "Genomic Organization of Mouse and Human 65 kDa FK506-binding protein  
 (FKBP65) genes and evolution of the FKBP Multigene Family.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF456413; AAL57621.1; -.  
 DR EMBL; AF456412; AAL57621.1; JOINED.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000886; ER target.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR Pfam; PF00036; ehand; 2.  
 DR Pfam; PF00254; FKBP; 4.  
 DR SMART; SM00054; EFh; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 1.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; UNKNOWN\_1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 4.  
 SQ SEQUENCE 581 AA; 64697 MW; FD6F777940AD91E9 CRC64;

Query Match 48.5%; Score 1022; DB 11; Length 581;  
 Best Local Similarity 55.8%; Pred. No. 1.2e-78;  
 Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLLGMVCGEKRIITIPFLAYGEDGDKDIPGQASLVFDVALLDLH 60  
 Db 202 TVVGSGLWIKGMDQGLLGMVCGEKRIITIPFLAYGEKGYGTIIPQAQSLVFVLLDVH 261  
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLRYHYNGTLLDGTLLFDSSYSRNRTFTYIGQYV 120  
 Db 262 NPKDVTQLETLELPQGVRRVAVAGDFMRHYNGSLMDGTLLFDSSYSRNHTYNTYVQGY 321  
 Qy 121 IFGMDGLLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHVIDFHNPSDSIS 179  
 Db 322 IFGMDGLQACIGERRITVPPHLYGENGTDGKI PGSAVLVFDIHVIDFHNPSDPVEI 381  
 Qy 180 TSHYKPPD-CSVLSKGGDYLYKHYNASLLDGTLLDSTNGLKTYNIVLGSQVVLGMDMG 238  
 Db 382 KTLSPENCNETSKIGDFIRYHNCNLLDGTLLFSSHYEAPQEI TLGANKVIEGLDRG 441  
 Qy 239 LQMCVGEKRTVIIPHLGYGAGVDGVP GSAVLVFDIELLELVAGLPEGYMFIWNGEV 298  
 Db 442 LQMCVGERRLITVPPHLAHGENGARG-VPGSAVLLEFEVLVSREDGLTGYLFWYQDP 500  
 Qy 299 SPNLFEEIN-----KVTFCCPFVSWRRWYPEGRGOL-PQDSNDSPPADL 342  
 Db 501 SYSLFEDMDLNKDGVEVPPPEFFSFIKAQVN-----EGKGRIMPQDDPKTISDM 549

## RESULT 7

```
Q9H6N5
ID Q9H6N5 PRELIMINARY; PRT; 481 AA.
AC Q9H6N5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA: FLJ22041.fis, clone HEP09061.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RL "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AK025694; BAB15220.1; -
DR HSSP; AK025694; BAB15220.1; -
DR SMART; O00688; 1PBK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFN; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 481 AA; 53219 MW; A4D5181BFC88BDFD CRC64;

Query Match 47.5%; Score 1000.5; DB 4; Length 481;
Best Local Similarity 55.1%; Pred. No. 6.2e-77;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY 1 TYGEGILIPGMKGLGCMVGKRIITIPPLAYGEGDGKIPGOASLFDVALLDLH 60
Db 102 TYVSGMLIKMGDQGLGCMVGKRIITIPPLAYGEGDGKIPGOASLFDVALLDLH 161
QY 61 NPKDSISENKVVPENCERISQSGDFLYHYNGTLLDGTLDSSYSRNRTPDTYIGQYV 120
Db 162 NPKDAVQLETLPPGCVRRAGAGDFMRHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 221
QY 121 IPGMDEGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLFDIHDVDFHNPDSISI 179
Db 222 IPGMDEGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLFDIHDVDFHNPDSISI 281
QY 180 TSHYKPPD-CSVLSKKGDLKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
Db 282 RTLSRPSETCNETTKLGDVRYHYNGSLDGTQLFTSHDYGAPOBATLGANKVIEGLDTG 341
QY 239 LREMCVGEKRTVIIPPHLYGEGAGVDGVPGSVAVLFDIELLELVAGLPEGMFTWNGEV 298
Db 342 LQGMCGERRQLIIVPPHLAGESGARG-VPGSAVLFFVELSVREDGLTGYLFWHKDP 400
QY 299 SPNLFE--EINK-----VTFPCFPVSWRRWYPEGSQL 330
Db 401 PANLFEDMDLNKDGVEPPEEFTFI-----KAQVSEKGRLL 436

RESULT 8
Q9H3N3
ID Q9H3N3 PRELIMINARY; PRT; 582 AA.
AC Q9H3N3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65kDa FK506-binding protein.
GN HFKBP65.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Q9H6N5
ID Q9H6N5 PRELIMINARY; PRT; 582 AA.
AC Q9H6N5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.2 kDa protein (65 kDa FK506-binding protein)
DE (EC 5.2.1.8).
GN FKBP65.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Mitsumori C., Morikawa N., Isogai T., Ota T., Yuri K., Nishikawa T.,
RA Masuho Y., Nagahara K.;
RL "The human 65kDa FK506-binding protein (hFKBP65) gene induces the
RL morphological differentiation of NT2 neuron precursor cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AB045981; BAB20974.1; -
DR HSSP; P20081; 1YAT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFN; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 582 AA; 64305 MW; 04B25129A1D4D92 CRC64;

Query Match 47.5%; Score 1000.5; DB 4; Length 582;
Best Local Similarity 55.1%; Pred. No. 8.1e-77;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY 1 TYGEGILIPGMKGLGCMVGKRIITIPPLAYGEGDGKIPGOASLFDVALLDLH 60
Db 203 TYVSGMLIKMGDQGLGCMVGKRIITIPPLAYGEGDGKIPGOASLFDVALLDLH 262
QY 61 NPKDSISENKVVPENCERISQSGDFLYHYNGTLLDGTLDSSYSRNRTPDTYIGQYV 120
Db 263 NPKDAVQLETLPPGCVRRAGAGDFMRHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 322
QY 121 IPGMDEGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLFDIHDVDFHNPDSISI 179
Db 323 IPGMDEGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLFDIHDVDFHNPDSISI 382
QY 180 TSHYKPPD-CSVLSKKGDLKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
Db 383 RTLSRPSETCNETTKLGDVRYHYNGSLDGTQLFTSHDYGAPOBATLGANKVIEGLDTG 442
QY 239 LREMCVGEKRTVIIPPHLYGEGAGVDGVPGSVAVLFDIELLELVAGLPEGMFTWNGEV 298
Db 443 LQGMCGERRQLIIVPPHLAGESGARG-VPGSAVLFFVELSVREDGLTGYLFWHKDP 501
QY 299 SPNLFE--EINK-----VTFPCFPVSWRRWYPEGSQL 330
Db 502 PANLFEDMDLNKDGVEPPEEFTFI-----KAQVSEKGRLL 537

RESULT 9
Q96AY3
ID Q96AY3 PRELIMINARY; PRT; 582 AA.
AC Q96AY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.2 kDa protein (65 kDa FK506-binding protein)
DE (EC 5.2.1.8).
GN FKBP65.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
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|  |  |
|--|--|
| DR   | InterPro; IPR002048; EF-hand.  |
| DR   | InterPro; IPR000886; ER-target.  |
| DR   | InterPro; IPR001179; FKBP_PPIase.  |
| DR   | Pfam; PF00036; ehand; 2.   |
| DR   | Pfam; PF00254; FKBP; 2.  |
| DR   | SMART; SM00054; Efh; 2.  |
| DR   | PROSITE; PS00018; EF_HAND; UNKNOWN_1.  |
| DR   | PROSITE; PS00014; ER_TARGET; UNKNOWN_1.  |
| DR   | PROSITE; PS50059; FKBP_PPIASE_3; 2.  |
| SQ   | SEQUENCE 355 AA; 38950 MW; DBECEF4B8618BF54F CRC64;  |
| <br>   |  |
| Query Match  | 32.7%; Score 688; DB 4; Length 355;  |
| Best Local Similarity  | 42.5%; Pred.No.1.8e-50;  |
| Matches 135; Conservative 50; Mismatches 51; Indels 82; Gaps             |  |
| <br>   |  |
| QY   | 87 LRVHYNGTLLDGLTFDSSYSRNRFTDTYIGQGVIIPGMDGLGVGCIGKRRIVVPPHLG 146<br>:     :     :     :     :     :     :     :     :     :     :           |
| Db   | 1 MEYHYNGSLMDGTLFDSSYSRNHTYNTYIGQGIIPGMDQLQCAGCAGERRITIPPHLA 60<br>:     :     :     :     :     :     :     :     :     :     :             |
| <br>   |  |
| QY   | 147 YGEGRGN----- 154<br>      :  |
| Db   | 61 YGEGTDSIGLQGSAPLRFRSGEQPSLGREGYGKTEPAYPDPAVLGASVSFPVKW 120<br>:     :     :     :     :     :     :     :     :     :     :               |
| <br>   |  |
| QY   | 155 -----IPGSALVFDPHVIDFNHPSDSISITSHYKPPD-CSVLSKKGDYLKYHN 203<br>:     :     :     :     :     :     :     :     :     :     :               |
| Db   | 121 ASHADPGDKIPGSALVIFNVHIDFNHPADVEIRTLSPSTCNETTKLGDFVRYHN 180<br>:     :     :     :     :     :     :     :     :     :     :              |
| <br>   |  |
| QY   | 204 ASLLDGTLLDTSWNMLGKTNYNLVGSGOVILGMDMGLREMCVGEKRTVIIIPPHLYGGEAV 263<br>:     :    :    :    :    :    :    :    :    :    :    :    :    : |
| Db   | 181 CSLLDGTQLFTSHDYGAPEATLGANKVIEGLDTGLQCMCVGERRLI VPHLAGESGA 240<br>:     :    :    :    :    :    :    :    :    :    :    :    :          |
| <br>   |  |
| QY   | 264 DGEVPGSALVFDTIELLELVAGLPEGVMFTWNEGVSNLFEE--EINK-----VTFF 312<br>:     :     :     :     :     :     :     :     :     :     :            |
| Db   | 241 RG-VGGSALLVFEVELVSREDGLPTGYLPVWHKDDPPANLFEEDMLNKDGVEPPEEFSTFI 299<br>:     :     :     :     :     :     :     :     :     :     :       |
| <br>   |  |
| QY   | 313 CCPFVSWRWYPYEGRGOL 330<br>:     :     :     :     :     :     :     :     :     :     :  |
| Db*  | 300 -----KAQVSEKGKRL 310<br>:     :     :     :     :     :     :     :     :     :     :  |
| <br>   |  |
| RESULT 11  |  |
| Q9UF89   | PRELIMINARY; PRT; 262 AA.  |
| ID Q9UF89  |  |
| AC Q9UF89  |  |
| DT 01-MAY-2000   | (TrEMBLrel. 13, Created)   |
| DT 01-MAY-2000   | (TrEMBLrel. 13, Last sequence update)  |
| DE 01-MAR-2002   | (TrEMBLrel. 20, Last annotation update)  |
| De Hypothetical 28.9 kDa protein (Fragment).                             |  |
| CN DKZP58610821.   |  |
| OS Homo sapiens (Human).   |  |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |  |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.            |  |
| OX NCBI_TaxId=9606;  |  |
| XP [1]   |  |
| RN SEQUENCE FROM N.A.  |  |
| RP TISSUE=UTERUS;  |  |
| RC Ottenwaelder H., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S. |  |
| RA Submitted (Nov-1999) to the EMBL/GenBank/DDJB databases.              |  |
| RL EMBL; AL33116; CAB61418.1; -.   |  |
| DR EMBL; Q00688; 1PBK.   |  |
| DR HSPG; Q00688; 1PBK.   |  |
| DR InterPro; IPR002048; EF-hand.   |  |
| DR InterPro; IPR000886; ER-target.                                       |  |
| DR Pfam; PF00036; ehand; 2.  |  |
| DR Pfam; PF00254; FKBP; 2.   |  |
| DR SMART; SM00054; Efh; 2.   |  |
| DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.                                 |  |
| DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.                               |  |
| DR PROSITE; PS50059; FKBP_PPIASE_3; 2._1                                 |  |
| KW Hypothetical protein.   |  |
| NON TER 1  |  |
| SQ SEQUENCE 262 AA; 28926 MW; A9630934276BA84E CRC64;                    |  |





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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Du Z., Le T.T.;
RT "The sequence of C. elegans cosmid C50F2.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80445; AAB37799.1; -.
DR HSSP; P20071; 1BL4.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00254; FKBP_2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_2.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 264 AA; 29937 MW; 90B79FD4FF978A2D CRC64;

Query Match 16.3%; Score 344; DB 5; Length 264;
Best Local Similarity 33.9%; Pred. No. 2.6e-21;
Matches 80; Conservative 45; Mismatches 95; Indels 16; Gaps 5;

QY 63 KDSISIEKVV---PENCERISQSGDFLRVHYNGTLLDGTGLFDSYSRNRTFDYIGQG 118
DB 25 KDEDGLIKIRPIKAECPIKSDQGDVLDQWYKLSDDKGKEIGSNFNK-KPYTFTLGKG 83
QY 119 YVIPGMEGLLGVCIGEKRRIVPPHLYGEG--RGNIPGSVAVLVFDIHVIDFH----- 171
DB 84 QVIPGMERAMTGMCKGKRRVVPGLNGFGDKGRERDNKEDQTLVYTVQLVDLFRVAVPG 143
QY 172 ---NPDSISITSHYK-PPDCSVLSKGDYLYKHYNASLLDGTGLDSTWNLGKTYNIVLG 227
DB 144 EKWTDEGIVIEQTHKIDEDCKKSKSGDTIHQQVVLHLEDGTFVDSFSRNAPFIFKLN 203
QY 228 SGQVVLGMDGLREMCVGEKRTVIIPPHLYGEGVGDGVPGSVAVLVFDIELLELV 283
DB 204 NNEVIKGMIDAMTGMCEGERQVIPSDFGYGDDGRAPAIPGKARLYFDITLEKLI 259

RESULT 15
Q95Q60 PRELIMINARY; PRT; 300 AA.
AC Q95Q60;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 34.2 kDa protein.
GN C50F2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Du Z., Le T.T.;
RT "The sequence of C. elegans cosmid C50F2.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80445; AAK68259.1; -.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_2.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34160 MW; A70252F2736CF36C CRC64;

Query Match 16.3%; Score 344; DB 5; Length 300;
Best Local Similarity 33.9%; Pred. No. 3.1e-21;
Matches 80; Conservative 45; Mismatches 95; Indels 16; Gaps 5;

QY 63 KDSISIEKVV---PENCERISQSGDFLRVHYNGTLLDGTGLFDSYSRNRTFDYIGQG 118
DB 61 KDEDGLIKIRPIKAECPIKSDQGDVLDQWYKLSDDKGKEIGSNFNK-KPYTFTLGKG 119
QY 119 YVIPGMEGLLGVCIGEKRRIVPPHLYGEG--RGNIPGSVAVLVFDIHVIDFH----- 171
DB 120 QVIPGMERAMTGMCKGKRRVVPGLNGFGDKGRERDNKEDQTLVYTVQLVDLFRVAVPG 179
QY 172 ---NPDSISITSHYK-PPDCSVLSKGDYLYKHYNASLLDGTGLDSTWNLGKTYNIVLG 227
DB 180 EKWTDEGIVIEQTHKIDEDCKKSKSGDTIHQQVVLHLEDGTFVDSFSRNAPFIFKLN 239
QY 228 SGQVVLGMDGLREMCVGEKRTVIIPPHLYGEGVGDGVPGSVAVLVFDIELLELV 283
DB 240 NNEVIKGMIDAMTGMCEGERQVIPSDFGYGDDGRAPAIPGKARLYFDITLEKLI 295

Search completed: April 26, 2003, 06:55:47
Job time : 35.1369 secs
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